Total tRNA: 18		Proteo	nics						Transcri	ptomics							
Leptospirillum	Lgth			AB10 A	B10	C10	C10	C10	G2E1	A-drift C75	R1.1	R1.1	RARP	R11	R11		
Group IV gene	(aa) BLAST Hit	Nov05_S Nov05_	M Aug07_S	GS0 G	S1	GS0	G\$0.5	GS1	GS2	GS0 GS1	GS0	G\$0.5	G\$0.5	GS0	G\$1	L3 gene	% id
UBABSL4_2423G0001	430 heavy metal efflux pump, CzcA family									0.0101						UBAL3_79160013	87
UBABSL4_2423G0002	279 peptide chain release factor 3		0.01557													UBAL3_79160012	81
UBABSL4_2423G0003	161 recombination protein RecR		0.02023							0.009						UBAL3_79160011	78
UBABSL4_2423G0004	559 DNA polymerase III, subunits gamma and tau		0.00388							0.0155						UBAL3_79160009	64
tRNA-Ser-GGA	tRNA Ser GGA																
UBABSL4_2423G0005	85 Conserved protein of unknown function		0.07664													UBAL3_79160008	48
UBABSL4_2423G0006	262 MscS Mechanosensitive ion channel									0.0275						UBAL3_79160005	71
UBABSL4_2423G0007	123 diguanylate cyclase															UBAL3_79160004	54
UBABSL4_2423G0007a	146 diguanylate cyclase															UBAL3_79160004	54
UBABSL4_2423G0008a	105 Conserved hypothetical protein																
UBABSL4_2423G0008	279 Transposase			1.0919	0.1439			0.24	2 0.1149		0.375	0.148	5 0.3375	1.1104	1.3595	5	
UBABSL4_2423G0009	288 hypothetical protein									0.01							
UBABSL4_2423G0009	288 Transposase									0.01							
UBABSL4_2423G0010	59 Transposase									0.0734			0.0532				
UBABSL4_2423G0011	118 Transposase			1.678				0.572	1 0.2716		0.3224	0.2633	3 0.4257	1.0154	1.2876		
UBABSL4_2423G0012	195 Conserved protein of unknown function									0.0592						UBAL3_92050079	79
UBABSL4_2423G0013	138 hypothetical protein																
UBABSL4_2423G0014	693 excinuclease ABC, B subunit									0.0125						UBAL3_92050081	85
UBABSL4_2423G0015	90 Conserved hypothetical protein									0.1603						UBAL3_92050082	65
UBABSL4_2423G0016	139 Transposase					0.2700	0.50/3	7		0.0208		0.010	_			UD 412 00050105	
UBABSL4_2423G0017	413 DNA (cytosine-5-)-methyltransferase					0.3628	0.5867	/		0.0629		0.012				UBAL3_92050195	65
UBABSL4_2423G0018	97 plasmid maintenance system antidote protein, XRE									0.0149		0.0534	4			UBAL3_44810054	64
UBABSL4_2423G0019	112 hypothetical protein	0.000	21 004411							0.000						LID & L 2 . 0.00 E 0.00 /	69
UBABSL4_2423G0021 UBABSL4_2423G0022	320 outer membrane efflux protein 174 efflux transporter, RND family, MFP subunit	0.020	31 0.04411							0.009						UBAL3_92050086 UBAL3_92050087	53
UBABSL4_2423G0022	243 acriflavin resistance protein									0.0059						UBAL3_92050088	33 86
UBABSL4 2423G0025	284 sigma-54factor,interactiondomain-containing									0.0037						UBAL3_80150010	51
UBABSL4_2423G0025	80 hypothetical protein															0BAL3_00130010	31
UBABSL4_2423G0027	310 6-phosphogluconate dehydrogenase NAD-binding																
tRNA-Thr-CGT	tRNA Thr CGT																
UBABSL4 2423G0028	334 Conserved protein of unknown function	0.18236 0.075	38 0.02601							0.0086						UBAL3_80150011	72
UBABSL4 2423G0029	399 Conserved protein of unknown function	0.10200 0.070	0.02001							0.0072						UBAL3_80150012	55
UBABSL4 2423G0030	135 Putative TPR-domain containing protein									0.0321						UBAL3 80150013	70
UBABSL4 2423G0031	52 hypothetical protein									0.1387							
UBABSL4_2423G0032	211 Putative carbohydrate kinase, PfkB family		0.29845							0.0137						UBAL3_80150014	77
UBABSL4_2423G0033	296 tRNA delta(2)-isopentenylpyrophosphate transferase	(EC 2.5.1.8)								0.0341						UBAL3_80150016	55
UBABSL4_2423G0034	509 DNA mismatch repair protein MutL									0.0057						UBAL3_80150017	55
UBABSL4_2423G0035	97 DNA mismatch repair protein MutL									0.0148						UBAL3_80150017	
UBABSL4_2423G0036	271 TPR domain-containing protein	0.37459 0.0	73 0.01603							0.0639						UBAL3_80150018	69
UBABSL4_2423G0037	96 Putative ToIB protein									0.0301						UBAL3_80150019	76
UBABSL4_11601G0001	559 translation elongation factor G	1.41648 1.07								0.0206						UBAL3_80420003	90
UBABSL4_11601G0002	400 translation elongation factor Tu	4.61891 4.779	44 4.92387							0.3282						UBAL3_80150009	97
UBABSL4_11601G0003	50 Ribosomal protein L33									0.0866						UBAL3_80150008a	94
tRNA-Trp-CCA	tRNA Trp CCA																
UBABSL4_11601G0004	64 preprotein translocase, SecE subunit									0.0451						UBAL3_80150008	70
UBABSL4_11601G0005	115 Transcription antitermination protein (NusG)		0.26436							0.1001						UBAL3_80150007	85
UBABSL4_11601G0006	100 Ribosomal protein \$10	0.13535 0.611								0.0431						UBAL3_80420005	94
UBABSL4_11601G0007	205 Ribosomal protein L3		78 0.45548							0.0985						UBAL3_80420006	78
UBABSL4_11601G0008	213 Ribosomal protein L4	0.109								0.1964						UBAL3_80420007	63
UBABSL4_11601G0009	96 Ribosomal protein L23	0.786								0.0570						UBAL3_80420008	91
UBABSL4_11601G0010	274 Ribosomal protein L2	0.39519 0.393								0.0579						UBAL3_80420009	91
UBABSL4_11601G0011	95 Ribosomal protein \$19	0.35619 0.889	77 0.605/3							0.0759						UBAL3_80420010	97
UBABSL4_11601G0012	25 Ribosomal protein L22		0.07207													UBAL3_80420011	97
UBABSL4_11601G0013	34 Ribosomal protein L22	0.41274 0.770	0.06387							0.043						UBAL3_80420011	97 91
UBABSL4_11601G0014 UBABSL4_11601G0015	229 Ribosomal protein \$3 139 Ribosomal protein L16/L10E	0.41374 0.769 0.58426 0.6598								0.063						UBAL3_80420012 UBAL3_80420013	91 92
UBABSL4_11601G0016	67 Ribosomal protein L29	U.JO426 U.659	0.34031													UBAL3_80420013	92 77
UBABSL4_11601G0016	90 Ribosomal protein \$17	0.15039 0.099								0.1443						UBAL3_80420015	77 76
0DAB3L4_11001G0017	70 Kibosoffidi profetti 317	0.13037 0.099	/2 0.22721							0.1443						UDAL3_00420013	/0

UD 4 DOL 4 12 (01 DOC)	100 80	0.075	0.466.7	0.50000								110 410 00 1005	
UBABSL4_11601G0018	123 Ribosomal protein L14			0.52081			0.0234					UBAL3_80420016	70
UBABSL4_11601G0019	Ribosomal protein L24	0.11602 0.		0.19488			0.0742					UBAL3_80420017	73
UBABSL4_11601G0020 UBABSL4_11601G0021	175 Ribosomal protein L5			0.59541			0.0742					UBAL3_80420018 UBAL3_80420019	87 96
UBABSL4_11601G0021	62 Ribosomal protein \$14 133 Ribosomal protein \$8	U.	.30013	0.37341			0.1952					UBAL3_80420019	96
UBABSL4_11601G0022	146 Ribosomal protein L6P/L9E			0.29747			0.0296					UBAL3_80420021	86
0BAB3E4_11001G0023	140 KIDOSOTTAL PROJEKT EST/E/E			0.2//4/			0.0270					0DAL5_00420021	00
UBABSL4_3535G0001	72 Putative metallo-beta-lactamase family protein											UBAL3_80290065	79
UBABSL4_3535G0002	218 Probable peptidyl-prolyl cis-trans isomerase						0.0265					UBAL3_80290064	83
UBABSL4_3535G0003	283 GTP-binding protein (TypA)	0.04783 0.	.35588	0.37215			0.0612					UBAL3_80290062	
UBABSL4_3535G0004	238 Conserved protein of unknown function						0.0242					UBAL3_80290061	
UBABSL4_3535G0004a	143 Conserved protein of unknown function	0.	.15092	0.205			0.0101					UBAL3_80290060	67
UBABSL4_3535G0005	346 Conserved hypothetical protein						0.0375						
UBABSL4_3535G0006	140 Conserved hypothetical protein											UBAL3_80290058	81
UBABSL4_3535G0007	246 Recombination protein O (RecO)											UBAL3_80290057	48
UBABSL4_3535G0008	326 GTP-binding protein (Era)			0.00666			0.0487					UBAL3_80290056	
UBABSL4_3535G0009	185 Putative short-chain dehydrogenase											UBAL3_80290048	58
UBABSL4_3535G0010	65 Putative short-chain dehydrogenase											UBAL3_80290048	56
UBABSL4_3535G0011	72 hypothetical protein						0.1603						
UBABSL4_3535G0012	65 hypothetical protein												
UBABSL4_3535G0013	59 hypothetical protein												
UBABSL4_3535G0014	205 Mannose-1-phosphate guanylyltransferase/mannose						0.0422					UBAL3_80290046	90
UBABSL4_3535G0015	136 Mannose-1-phosphate guanylyltransferase/mannose	e-6-phosphat	e isom				0.0955					UBAL3_80290046	90
UBABSL4_3535G0016	478 Phosphomannomutase (EC 5.4.2.8) 335 Long-chain-fatty-acidCoA ligase (EC 6.2.1.3)			0.04543			0.0543 0.0043					UBAL3_80290045 UBAL3_80290044	71
UBABSL4_3535G0017 UBABSL4_3535G0019	163 Long-chain-fatty-acidCoA ligase (EC 6.2.1.3)					0.2298	0.0043					UBAL3_00290044	
UBABSL4_3535G0019	762 Conserved hypothetical protein					0.2270						UBAL3_80290035	44
UBABSL4_3535G0020	261 Conserved hypothetical protein	0.31116 0.	15849	0.09548								UBAL3_80290038	87
05/15024_0000000021	201 Conserved by Contened protein	0.01110 0.	.10047	0.07000								05/120_002/0000	07
UBABSL4_6391G0001	330 hypothetical protein								0.0314	0.019	0.1919 0.	1987	
UBABSL4_6391G0002	235 Transposase										0.2327 0.	2137 UBAL3_48660070	73
UBABSL4_6391G0003	368 Transposase							0.0086			0.2279 0.	2139 UBAL3_48660069	63
UBABSL4_6391G0004	129 hypothetical protein										0.0929 0.	0932	
UBABSL4_6391G0005	181 hypothetical protein										0.2459 0.	1812	
UBABSL4_6391G0006	49 hypothetical protein						0.0883				0.1397 0.	1562	
UBABSL4_6391G0007	79 hypothetical protein										0.0867 0.		
UBABSL4_6391G0008	75 hypothetical protein										0.0685 0.		
UBABSL4_6391G0009	185 hypothetical protein						0.2417	0.0171	0.028		0.5644 0.		
UBABSL4_6391G0010	171 Phage regulatory protein, Rha family							0.0185				1215 UBAL3_44810056	63
UBABSL4_6391G0011	154 Phage regulatory protein, Rha family							0.0206	0.0000			1278 UBAL3_44810056	90
UBABSL4_6391G0012	256 hypothetical protein								0.0202	0.0123	0.1471 0.0		
UBABSL4_6391G0013 UBABSL4_6391G0014	94 hypothetical protein 201 hypothetical protein									0.0154	0.091 0.0		
UBABSL4_6391G0015	97 hypothetical protein										0.12// 0.0		
UBABSL4_6391G0016	441 hypothetical protein						0.0164		0.0117		0.0002 0.		
UBABSL4_6391G0017	65 Conserved hypothetical protein						0.3329		0.0117		0.4477 0.		
UBABSL4_6391G0018	318 Conserved protein of unknown function	0.	.01131		0.2874		1.3927	0.01	0.0651			8909 UBAL3_93200053	39
UBABSL4 6391G0019	172 Conserved hypothetical protein						0.0084				0.01 0.0		
UBABSL4_6391G0020	158 Conserved hypothetical protein				0.5784		0.2191	0.0201	0.0328	0.0199	0.7583 0.		
UBABSL4_6391G0021	186 hypothetical protein						0.1396				0.5061 0.3	2821	
UBABSL4_7009G0001	62 hypothetical protein												
UBABSL4_7009G0002	110 Conserved protein of unknown function						0.0393					UBAL3_80630042	53
UBABSL4_7009G0003	185 Putative flagellar motor protein (OmpA/MotB)						0.0156					UBAL3_80630043	69
UBABSL4_7009G0004	198 Putative flagellar motor component (MotA)						0.0219					UBAL3_80630044	85
UBABSL4_7009G0005	121 putative CheW protein	0.16779 0.	.68372	0.28714								UBAL3_80630045	87
UBABSL4_7009G0006	57 putative CheW protein	0.000 -	00/07	0.11055								UBAL3_80630045	
UBABSL4_7009G0007	440 methyl-accepting chemotaxis sensory transducer	0.323 0.					0.0262					UBAL3_80630046	80
UBABSL4_7009G0008	Putative signal transduction histidine kinase (CheA)	0.06622 0.					0.0367					UBAL3_80630047	84
UBABSL4_7009G0009	140 Putative signal transduction histidine kinase (CheA)			0.10857			0.103					UBAL3_80630047	07
UBABSL4_7009G0010	128 Putative response regulator receiver protein (CheY)	0.42298 0.	.471//	1.13664		0.3858	0.0338 0.0459					UBAL3_80630048	96
UBABSL4_7009G0011 UBABSL4_7009G0012	157 Transposase 58 Conserved hypothetical protein					0.3638	0.0459						
UBABSL4_7009G0012	123 Transposase												
00/10014_/00/00013	120 (14)(15)(03)(30)												

UBABSL4_7009G0014 UBABSL4_7009G0015 UBABSL4_7009G0016 UBABSL4_7009G0017 UBABSL4_7009G0018 UBABSL4_7009G0022 UBABSL4_7009G0023 UBABSL4_7009G0024	246 RNA polymerase, sigma 28 subunit 117 Probable cobyrinic acid a,c-diamide synthase 333 flagellar biosynthesis protein FlhA 451 flagellar biosynthetic protein FlhB 154 Flagellar biosynthetic protein FliR 173 flagellar biosynthetic protein FliP 108 Conserved protein of unknown function										0.0293 0.0217 0.0224 0.0169 0.0167	UBA UBA UBA UBA UBA UBA	L3_80630049 L3_80630050 L3_80630051 L3_80630052 L3_80630053 L3_80630054 L3_80630056 L3_80630057	75 84 69 86 75 80 94 66
UBABSL4_10842G0001	983 exodeoxyribonuclease V, gamma subunit			0.00442							0.0411	LIRA	L3_78890003	46
UBABSL4_10842G0002	151 CO dehydrogenase beta subunit/acetyl-CoA synthase e	epsilon s	ubunit	0.00442							0.0411		L3_78890002	88
UBABSL4_10842G0003	110 Conserved hypothetical protein												L3_78890001	44
UBABSL4_10842G0004	190 CO dehydrogenase beta subunit/acetyl-CoA synthase e	epsilon		0.00000							0.0007		L3_78890002	68
UBABSL4_10842G0005 UBABSL4_10842G0006	341 <mark>6-phosphogluconatedehydrogenase,</mark> 514 Putative multi-sensor histidine kinase		0.052/4	0.38208							0.0296 0.0028		L3_79800001 L3_69480006	79 69
UBABSL4_10842G0007	229 two component transcriptional regulator, winged helix fa	vlimp									0.0026		L3_69480007	78
UBABSL4 10842G0008	145 Conserved protein of unknown function	,									0.0398		L3 69480008	63
UBABSL4_10842G0009	271 Putative molybdopterin biosynthesis protein			0.04006							0.0426	UBA	L3_69480009	90
UBABSL4_10842G0010	81 Conserved protein of unknown function		0.33305	0.28149								UBA	L3_69480010	81
UBABSL4_10842G0011	94 Putative ThiS family protein			0.03465							0.0307		L3_69480011	84
UBABSL4_10842G0012	•	.15487	0.04939	0.18634							0.0561		L3_69480012	91
UBABSL4_10842G0013 UBABSL4_10842G0014	117 Putative ThiF family protein 68 cysteine synthase										0.0123		L3_69480013 L3_69480014	85 84
UBABSL4_10842G0015	210 cysteine synthase										0.0275		L3_69480014	79
UBABSL4_10842G0016	69 thiamine biosynthesis protein ThiS										0.0418		L3_69480015	71
UBABSL4_10842G0017	222 adenosylhomocysteinase		0.29164	0.23965							0.1105	UBA	L3_69480016	91
UBABSL4_10842G0018	75 hypothetical protein													
UBABSL4_10842G0019	93 hypothetical protein	01.405	0.00547	0.10050							0.0071	LIDA	12 (040001/	
UBABSL4_10842G0020 UBABSL4_10842G0021				0.18958 0.53162							0.2061 0.1682		L3_69480016 L3_69480017	92
OB/\B3E4_10042\O0021	3-ddenosymmenhomme symmendse	./0151	0.01007	0.55102							0.1002	OBA	25_07400017	72
UBABSL4_12259G0001	66 hypothetical protein											0.048 0.0785 0.0476 0.0166		
UBABSL4_12259G0002	230 Conserved hypothetical protein				0.2649					0.1393	0.0125		L3_96120048	100
UBABSL4_12259G0003	93 hypothetical protein										0.0100	0.0557 0.1013 0.0184 0.0588		
UBABSL4_12259G0004 UBABSL4_12259G0005	134 hypothetical protein 535 hypothetical protein				0.0569		0.07			U U866	0.0108 0.0647	0.0946		
UBABSL4_12259G0006	225 hypothetical protein				0.0307		0.07			0.0077	0.0047	0.2677 0.2071 0.1953 0.0076 0.102		
UBABSL4_12259G0007	275 Putative filamentous haemagglutinin family protein				0.1108						0.0315		L3_78920045	54
UBABSL4_12259G0008	158 Putative filamentous haemagglutinin family protein										0.1735	0.2408 1.0161 0.3974 0.7042 2.629 UBA	L3_78920045	59
UBABSL4_12259G0009	141 hypothetical protein				0.5401						0.1228	0.2923		
UBABSL4_12259G0010	238 icmL/dotl				0.064				0.7001		0.1273	0.2398 0.7398 0.3034 1.2586 4.2622		
UBABSL4_12259G0011 UBABSL4_12259G0012	225 hypothetical protein 93 Conserved hypothetical protein				0.2031	0.4317	0.8054		0.6001	0.5698	0.2052	0.155		
UBABSL4_12259G0013	294 Conserved hypothetical protein				1.1398		0.0036	0.206		0.218	0.1700	0.9059 0.5989 0.5873 1.1702 1.6731		
UBABSL4_12259G0014	482 hypothetical protein		0.03358	0.00451	0.632		0.2332			0.4987		0.4473 0.3868 0.3322 0.9269 1.2881		
UBABSL4_12259G0015	652 Conserved hypothetical protein				0.1402				0.1035	0.1966	0.0996	0.4036 0.3654 0.313 0.4752 1.0864 UBA	L3_95390007	23
UBABSL4_12259G0016	358 hypothetical protein				0.2978		0.2093			0.179	0.1007	0.2303 0.3761 0.1841 0.5403 1.4137		
UBABSL4_12259G0017	273 N-6 DNA methylase				0.1674						0.0634	0.1858 0.0759 0.1725 0.2884 0.3243		
UBABSL4_12259G0018 UBABSL4_12259G0019	336 type I restriction-modification system methyltransferase su 172 hypothetical protein	ubunit			0.0907 0.2657						0.0258 0.0252	0.0566 0.1121 0.2445 0.257 0.0553 0.0301 0.3468 0.2985 0.4004		
UBABSL4_12259G0020	90 hypothetical protein				0.2637						0.0232	0.0705 0.1726 0.0698 0.0951 0.2672		
UBABSL4_12259G0021	301 DNA-cytosine methyltransferase (EC:2.1.1.37)				0.3036					0.6389		0.0632 0.1356 0.0569 0.0872		
UBABSL4_8849G0001	215 glucose-1-phosphate adenylyltransferase										0.1342		L3_94530083	85
UBABSL4_8849G0002	80 glucose-1-phosphate adenylyltransferase	0.40.45		0.02714							0.1057		L3_94530083	07
UBABSL4_8849G0003 UBABSL4_8849G0004	437 ATP synthase F1, beta subunit 2. 48 hypothetical protein	.94245	4.22661	2.83239							0.1056 0.0301	UBA	L3_94530086	97
UBABSL4_8849G0005	293 ATP synthase F1, gamma subunit		0.15345	0.2631							0.0301	IIRA	L3_94530087	87
UBABSL4_8849G0006	64 ATP synthase F1, alpha subunit			0.50894							0.0225		L3_94530088	67
UBABSL4_8849G0007	367 ATP synthase F1, alpha subunit	0.7745	0.83798	0.76328							0.0236		L3_94530088	
UBABSL4_8849G0008	204 Putative ATP synthase F1, delta subunit			0.12774							0.1344		L3_94530089	50
UBABSL4_8849G0009	147 ATP synthase FO, B subunit	F1 / / 2		0.04432	0.1000	0 (100	0.00:-	0.410:	1.5.11	1 4:30	0.1276		L3_94530090	82
UBABSL4_8849G0009a		.51661		0.29009 1.38186								3.219 2.2929 1.4378 4.1943 1.502 UBA 1.4 1.2779 1.1415 3.5123 1.2918 UBA	L3_94530090	82 100
UBABSL4_8849G0010	77 All Syllinuse FU, C SUDUNIT U.	.5515/	0.40702	1.30106	7.317	1.0420	1.4373	1.5/33	4.3038	0.0323	0.2023	1.4 1.2//7 1.1413 3.3123 1.2918 UBA	LJ_74JJUU71	100

UBABSL4_8849G0011 UBABSL4_8849G0012 UBABSL4_8849G0013 UBABSL4_8849G0014 UBABSL4_8849G0015 UBABSL4_8849G0016 UBABSL4_8849G0017	245 ATP synthase F0, A subunit 76 Conserved hypothetical protein 242 Conserved hypothetical protein 102 Conserved hypothetical protein 259 Conserved hypothetical protein 227 transposase			0.0648 0.038 0.006	UBAL3_94530092 UBAL3_94530093 UBAL3_95530023 UBAL3_95530022	86 74 63 71
UBABSL4_8849G0019 UBABSL4_8849G0019	131 transposase165 Phosphoglycolate phosphatase (EC 3.1.3.18)171 Probable membrane protein				UBAL3_94530097 UBAL3_94530096	62 63
UBABSL4_13011G0001	92 radical SAM family protein				UBAL3_95950042	77
UBABSL4_13011G0001	106 Conserved hypothetical protein				UBAL3_95950042	71
UBABSL4_13011G0003	329 Chemotaxis protein (CheV)	0.10386	0.0957	0.0438	UBAL3_95950044	86
UBABSL4_13011G0004	214 methyl-accepting chemotaxis sensory transducer			0.027	UBAL3_96120012	82
UBABSL4_13011G0005	250 metallo-beta-lactamase family protein		0.05212	0.0462	UBAL3_96120013	92
UBABSL4_13011G0006	, , ,	0.25692	0.18557	0.0221	UBAL3_95950046	74
UBABSL4_13011G0007	266 glycogen debranching enzyme GlgX				UBAL3_94530062	68
UBABSL4_13011G0008 UBABSL4_13011G0009	460 glycogen debranching enzyme GlgX 89 Conserved hypothetical protein				UBAL3_94530062 UBAL3_95680133	47
UBABSL4_13011G0007	265 Putative catalytic LigB subunit of aromatic ring-opening dioxyg	nenase		0.0163	UBAL3_95950049	66
UBABSL4_13011G0011	376 Methyltransferase	,0		0.0038	UBAL3_95950050	50
UBABSL4_13011G0012	427 histidyl-tRNA synthetase	0.00842	0.08645	0.0203	UBAL3_95950051	58
UBABSL4_13011G0013	443 Iron-sulfur protein			0.0554	UBAL3_95950052	76
UBABSL4_13011G0014	91 Conserved hypothetical protein			0.1268	UBAL3_95950053	69
UBABSL4_13011G0015	197 Probable cytochrome C oxidase			0.0439	UBAL3_95950054	89
UBABSL4_13011G0016 UBABSL4_13011G0017	374 Conserved protein of unknown function 135 Probable cytochrome-c oxidase			0.0347 0.0855	UBAL3_95950055 UBAL3_95950056	82 85
UBABSL4_13011G0018	147 Conserved protein of unknown function			0.0000	UBAL3_95950057	73
UBABSL4_13011G0019	71 Conserved protein of unknown function				UBAL3_95950058a	82
UBABSL4_13011G0020	50 Conserved protein of unknown function				UBAL3_95950059	88
UD 4 DOL 4 0007 00001	000 400 01			0.015	110 410 0 41 70000	7.4
UBABSL4_8997G0001 UBABSL4_8997G0002	280 ABC-2 type transporter 164 Conserved protein of unknown function		0.10593	0.0155 0.0088	UBAL3_94170028 UBAL3_94170029	76 83
UBABSL4_8997G0003	355 signal peptide peptidase SppA, 36K type		0.10373	0.0080	UBAL3_94170030	71
UBABSL4_8997G0004	222 Putative hydroxypyruvate reductase/glycerate kinase			0.0065	UBAL3_94170032	46
UBABSL4_8997G0005	371 Conserved protein of unknown function			0.0078	UBAL3_94170034	60
UBABSL4_8997G0006	115 Conserved protein of unknown function			0.0125	UBAL3_94170035	58
UBABSL4_8997G0007	223 Conserved protein of unknown function			0.0518	UBAL3_94170036	42
UBABSL4_8997G0008	121 Conserved protein of unknown function				UBAL3_94170037	46
UBABSL4_8997G0009 UBABSL4_8997G0010	128 Conserved hypothetical protein 410 major facilitator superfamily transporter				UBAL3_94170038 UBAL3_94170039	84 42
UBABSL4_8997G0011	157 CBS domain containing protein		0.24205	0.0368	UBAL3_94170040	69
UBABSL4_8997G0012	185 Conserved protein of unknown function			0.0702	UBAL3_94170041	48
UBABSL4_8997G0013	125 histidine triad (HIT) protein				UBAL3_94170042	80
UBABSL4_8997G0013a	165 Conserved protein of unknown function			0.2186	UBAL3_94170043	96
UBABSL4_8997G0014	88 Conserved protein of unknown function	0.01054		0.1475	UBAL3_94170043	96
UBABSL4_8997G0015 UBABSL4_8997G0016	194 Uracil phosphoribosyltransferase 333 aspartate carbamoyltransferase	0.01854	0.01956	0.0521 0.0087	UBAL3_94170044 UBAL3_94170045	73 79
UBABSL4_8997G0017	228 dihydroorotase	0.01578	0.02381	0.0063	UBAL3_94170046	72
UBABSL4_8997G0018	127 carbamoyl-phosphate synthase, small subunit			0.1363	UBAL3_94170047	61
UBABSL4_7601G0001	169 Conserved protein of unknown function			0.0085	UBAL3_24060060	68
UBABSL4_7601G0003	451 Putative TPR-domain containing protein	0.00798	0.00481	0.0352	UBAL3_24060058	/0
UBABSL4_7601G0004 UBABSL4_7601G0005	145 Putative TPR-domain containing protein 363 Putative DegT/DnrJ/EryC1/StrS aminotransferase			0.0298 0.0119	UBAL3_24060058 UBAL3_24060057	69 70
UBABSL4_7601G0006	218 Probable dethiobiotin synthase			V.VIII/	UBAL3_24060056	58
UBABSL4_7601G0007	257 Exodeoxyribonuclease III (EC 3.1.11.2)			0.0225	UBAL3_24060055	71
UBABSL4_7601G0008	172 Probable cation transport protein		0.03787	0.0335	UBAL3_24060054	67
UBABSL4_7601G0009	233 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.1			0.0062	UBAL3_24060053	60
UBABSL4_7601G0010	124 Putative methylenetetrahydrofolate reductase	0.05802	0.01751	0.0349	UBAL3_24060052	81
UBABSL4_7601G0011 UBABSL4_7601G0012	193 Putative methylenetetrahydrofolate reductase	0.0201	0.05063 0.25964	0.0523 0.0549	UBAL3_24060052 UBAL3_24060051	85 85
UBABSL4_7601G0012	184 Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) 383 Conserved hypothetical protein	0.0371	0.23704	0.00349	UBAL3_24060049	85 75
UBABSL4_7601G0016	183 Conserved hypothetical protein				3220_2 .0000 ./	. 0

UBABSL4_7601G0017 UBABSL4_7601G0018	91 GTP cyclohydrolase I (EC 3.5.4.16) 99 GTP cyclohydrolase I (EC 3.5.4.16)				0.047 0.014		UBAL3_24060046 UBAL3_24060046	98 82
UBABSL4_7601G0019 UBABSL4_7601G0020	210 5-formyltetrahydrofolate cyclo-ligase 279 N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)				0.010	03	UBAL3_24060045 UBAL3_24060044	58 75
UBABSL4_8072G0001	168 Conserved protein of unknown function						UBAL3_90980012	48
UBABSL4_8072G0002 UBABSL4_8072G0003	241 glutamyl-tRNA synthetase 194 glutamyl-tRNA synthetase			0.06758 0.02239	0.01	2	UBAL3_90980011 UBAL3_90980011	60
UBABSL4_8072G0004	167 Conserved hypothetical protein			0.02237	0.008	36	UBAL3_90980010	89
UBABSL4_8072G0005	260 Conserved protein of unknown function			0.02050	0.101		UBAL3_90980009	55
UBABSL4_8072G0006 UBABSL4_8072G0007	71 Probable pyruvate:ferredoxin oxidoreductase epsilon 223 Pyruvate:ferredoxin oxidoreductase gamma subunit		1.5162	0.03058 1.17826	0.121 ⁻ 0.226		UBAL3_90980006a UBAL3_90980006	90 91
UBABSL4_8072G0008	298 Putative pyruvate:ferredoxin oxidoreductase beta sul	0.29523		0.45179	0.663		UBAL3_90980005	96
UBABSL4_8072G0009	282 Pyruvate:ferredoxin oxidoreductase alpha subunit (EC	0.95995	0.86735	0.72383	0.327		UBAL3_90980004	95
UBABSL4_8072G0010 UBABSL4_8072G0011	128 hypothetical protein 135 Conserved protein of unknown function		0.02664	0.08043	0.157	8	UBAL3_90980003	71
UBABSL4_8072G0012	95 Conserved protein of unknown function				0.045	56	UBAL3_90980002	90
UBABSL4_8072G0013	212 heat shock protein DnaJ domain protein				0.020		UBAL3_90980001	65
UBABSL4_8072G0014 UBABSL4_8072G0015	109 Conserved protein of unknown function 114 Conserved protein of unknown function		0.0631	0.01905	0.013 0.050		UBAL3_79520072 UBAL3_79520072	58 76
UBABSL4_8072G0016	74 hypothetical protein					0.0424		
LIDARCI A 11757C0001	110 Canage and by weath attend protein							
UBABSL4_11757G0001 UBABSL4_11757G0002	119 Conserved hypothetical protein 157 Conserved hypothetical protein				0.036	58		
UBABSL4_11757G0003	196 O-methyltransferase family protein				0.007			
UBABSL4_11757G0004	205 GCN5-related N-acetyltransferase				0.014	41		
UBABSL4_11757G0005 UBABSL4_11757G0006	119 glyoxalase family protein59 Glyoxalase/bleomycin resistance						UBAL3_48660039	53
UBABSL4_11757G0007	150 flavin-nucleotide-binding protein-like						UBAL3_48660038	67
UBABSL4_11757G0008	93 hypothetical protein							
UBABSL4_11757G0009 UBABSL4_11757G0010	125 metallo-beta-lactamase family protein 52 Conserved hypothetical protein				0.027	77		
UBABSL4_11757G0011	73 hypothetical protein				0.07			
UBABSL4_11757G0012	94 addiction module toxin, RelE/StbE family				0.04			
UBABSL4_11757G0013 UBABSL4_11757G0014	68 hypothetical protein 119 transcriptional regulator-like				0.021 0.024		UBAL3_95680030	45
UBABSL4_11757G0015	144 transposase				1.021		05/125_75000050	40
UBAB\$L4_11757G0016	85 hypothetical protein							
UBABSL4_1871G0001	193 hypothetical protein				0.037	74		
UBABSL4_1871G0002	184 metallophosphoesterase				0.007		UBAL3_95660013	87
UBABSL4_1871G0002a	123 Conserved hypothetical protein				0.070)4		
UBABSL4_1871G0003 UBABSL4_1871G0004	88 nucleotidyltransferase substrate binding 105 DNA polymerase, beta domain protein region				0.013	37 2.3056	UBAL3_82700041 UBAL3_95660006	69 82
UBABSL4_1871G0005	169 Putative uracil-DNA glycosylase				0.0.0	2.0000	02/120_/0000000	02
UBABSL4_1871G0006	380 glycine oxidase ThiO				0.053		UBAL3_95450101	69
UBABSL4_1871G0006a UBABSL4_1871G0007a	85 UDP-glucose 6-dehydrogenase 76 UDP-glucose 6-dehydrogenase				0.067 0.056		UBAL3_95450100 UBAL3_95450100	77 77
UBABSL4_1871G0007	132 Conserved protein of unknown function				0.032		UBAL3_95450099	42
UBABSL4_1871G0008	241 sugar fermentation stimulation protein				0.029	29	UBAL3_95450098	68
UBABSL4_1871G0009 UBABSL4_1871G0010	275 HipA toxin/antitoxin 113 hypothetical protein				0.012	28		
UBABSL4_1871G0011	83 hypothetical protein				0.069			
UBABSL4_1871G0012	351 Conserved protein of unknown function						UBAL3_96120037	33
UBABSL4_3175G0001	202 cobalamin biosynthesis CbiG			0.0215			UBAL3_79520030	72
UBABSL4_3175G0002	87 Precorrin-6y C5,15-methyltransferase, CbiT			0.0210	0.016	56	UBAL3_79520029	63
UBABSL4_3175G0003	227 Precorrin-6y C5,15-methyltransferase, CbiE	0.04055	0.0453-	0.100.17		-	UBAL3_79520028	49
UBABSL4_3175G0004 UBABSL4_3175G0005	279 cobalamin biosynthesis protein CbiD 77 cobalamin biosynthesis protein CbiD	0.04851	0.04512	U.19847	0.005 0.05		UBAL3_79520027 UBAL3_79520027	66
UBABSL4_3175G0006	105 Ribosomal protein L9		0.08564	0.18613	0.03		UBAL3_79520027	65
UBABSL4_3175G0007	45 Ribosomal protein L34					-	UBAL3_79520025	91
UBABSL4_3175G0008 UBABSL4_3175G0009	108 Conserved protein of unknown function 415 Putative inner-membrane protein			0.02878	0.106	59	UBAL3_79520024a UBAL3_79520024	63 63
0B/D3E4_31/3G0007	Tio I dialize lillier-membrane profess			0.02070			UDALS_/ 7520024	oo.

UBABSL4_3175G0010 UBABSL4_3175G0011 UBABSL4_3175G0012 UBABSL4_3175G0013 UBABSL4_3175G0014 UBABSL4_3175G0015	445 tRNA modification GTPase TrmE 611 glucose inhibited division protein A 199 glucose inhibited division protein B 188 Cobyrinic acid a,c-diamide synthase, CbiA 288 parB-like partition protein 41 Conserved protein of unknown function	0.43865 0.68852	0.0097 0.0047		UBAL3_79520023 UBAL3_79520022 UBAL3_79520021 UBAL3_79520020 UBAL3_79520019 UBAL3_79520018	54 71 48 78 61 88
UBABSL4_3522G0001 UBABSL4_3522G0002 UBABSL4_3522G0003 UBABSL4_3522G0004 UBABSL4_3522G0005 UBABSL4_3522G0006 UBABSL4_3522G0007	120 Putative diguanylate phosphodiesterase 150 DNA topoisomerase III (EC 5.99.1.2) 512 DNA topoisomerase III (EC 5.99.1.2) 143 Conserved hypothetical protein 133 Single-strand DNA-binding protein 78 Conserved hypothetical protein 64 hypothetical protein			0.0123 0.0334 0.00	UBAL3_44810024 UBAL3_44810025 85 UBAL3_44810025 UBAL3_44810026 UBAL3_44810029 UBAL3_44810029	73 84 89 78 80
UBABSL4_3522G0008 UBABSL4_3522G0009 UBABSL4_3522G0010	370 DNA repair protein RadC 71 hypothetical protein 410 Conserved protein of unknown function			0.025	UBAL3_44810030 UBAL3_44810031	74 88
UBABSL4_3522G0011 UBABSL4_3522G0012 UBABSL4_3522G0013 UBABSL4_3522G0014 UBABSL4_3522G0015	322 Conserved hypothetical protein 57 hypothetical protein 155 Conserved hypothetical protein 84 Putative conjugal transfer protein (Trbl) 188 Putative conjugal transfer protein (Trbl)		0.0169		UBAL3_44810033 UBAL3_44810034 UBAL3_44810034	82 96 97
UBABSL4_3918G0001 UBABSL4_3918G0002 UBABSL4_3918G0004 UBABSL4_3918G0005 UBABSL4_3918G0007 UBABSL4_3918G0008 IRNA-Arg-ACG UBABSL4_3918G0009 UBABSL4_3918G0009 UBABSL4_3918G0010	291 integral membrane protein MviN 35 Ribosomal protein S20 214 Probable DNA polymerase III, delta subunit 76 Conserved protein of unknown function 118 Conserved protein of unknown function 262 Leucyl-tRNA synthetase (EC 6.1.1.4) 578 Leucyl-tRNA synthetase (EC 6.1.1.4) tRNA Arg ACG 200 Conserved hypothetical protein 135 hypothetical protein		0.0198 0.1225 0.0067 0.033 0.0549		UBAL3_96270003 UBAL3_78920001 UBAL3_78920002 UBAL3_78920003 UBAL3_78920003 UBAL3_78920004 UBAL3_78920004	74 89 60 76 77 65 70
UBABSL4_3918G0011 UBABSL4_3918G0012 UBABSL4_3918G0013 UBABSL4_3918G0014 UBABSL4_3918G0015	103 hypothetical protein 50 hypothetical protein 142 hypothetical protein 322 Conserved hypothetical protein 85 Conserved hypothetical protein			0.0121		
UBABSL4_11208G0001 UBABSL4_11208G0002 UBABSL4_11208G0003 UBABSL4_11208G0004 UBABSL4_11208G0005	201 Probable transposase 252 IstB domain protein ATP-binding protein 214 Conserved hypothetical protein 105 Resolvase helix-turn-helix domain protein 63 hypothetical protein		0.0067		UBAL3_80630090 UBAL3_95530028 UBAL3_95530029 UBAL3_95530030	47 85 82 59
UBABSL4_11208G0006 UBABSL4_11208G0007 UBABSL4_11208G0008	377 Putative potassium channel protein 71 Conserved hypothetical protein 229 Probable cyclic nucleotide-binding protein		0.0378		UBAL3_78920114 UBAL3_78920115 UBAL3_78920116	66 74 74
UBABSL4_11208G0009 UBABSL4_11208G0010 UBABSL4_11208G0011 UBABSL4_11208G0012	520 Putative competence protein (ComEC) 403 Phosphoglucosamine mutase (EC 5.4.2.10) 231 Conserved protein of unknown function 208 Conserved protein of unknown function	0.01616	0.0036		UBAL3_78920117 UBAL3_78920118 UBAL3_78920119 UBAL3_78920120	81 51 75
UBABSL4_11208G0013 UBABSL4_11208G0014 UBABSL4_11208G0015	54 hypothetical protein 284 Dihydropteroate synthase (EC 2.5.1.15) 23 hypothetical protein		0.0152		UBAL3_78920121	61
UBABSL4_12514G0001 UBABSL4_12514G0002 UBABSL4_12514G0003 UBABSL4_12514G0004 UBABSL4_12514G0005	185 Diguanylate cyclase/phosphodiesterase with PAS/PAC senso 346 diguanylate cyclase/phosphodiesterase with PAS/PAC senso 579 Conserved hypothetical protein 93 hypothetical protein 69 hypothetical protein				UBAL3_44810003 UBAL3_94530058	45 36
UBABSL4_12514G0006 UBABSL4_12514G0007 UBABSL4_12514G0008 UBABSL4_12514G0009	43 transposase 99 hypothetical protein 536 outer membrane efflux protein 302 Secretion protein (HIyD)		0.0296 0.0048		UBAL3_80420067 UBAL3_80420066	65 80

UBABSL4_12514G0010	128 ABC transporter ATP-binding protein								UBAL3_80420065	69
UBABSL4_12514G0011	297 ABC transporter ATP-binding protein								UBAL3_80420065	69
UBABSL4_12514G0012	99 ABC transporter ATP-binding protein					0.0076			UBAL3_80420065	69 84
UBABSL4_12514G0013 UBABSL4_12514G0014	381 Putative ABC transporter permease protein 335 Putative ABC transporter permease protein					0.0076			UBAL3_80420064 UBAL3_80420063	82
UBABSL4_12514G0015	42 hypothetical protein								0DAL3_00420003	02
UBABSL4_12854G0001	52 Cytochrome 572					2.9408	0.3984 0.1811		UBAL3_96270029	87
UBABSL4_12854G0002	80 hypothetical protein									
UBABSL4_12854G0003	122 hypothetical protein						0.0257	0.014	0.009	
UBABSL4_12854G0004	68 hypothetical protein					0.007	0.00.40	0.04070	01/0	
UBABSL4_12854G0005	270 hypothetical protein					0.0267			.0162	
UBABSL4_12854G0006 UBABSL4_12854G0007	153 hypothetical protein 167 hypothetical protein					0.0283	0.1015 0.0205 0.0564	0.0447 0	.0206	
UBABSL4_12854G0008	224 Conserved hypothetical protein						0.0364	0.0304 0	.0098 UBAL3_96270025	31
UBABSL4_12854G0009	220 Conserved protein of unknown function					0.0131	0.0432 0.0235 0.0143		0.005 UBAL3_69480063	32
UBABSL4 12854G0010	201 hypothetical protein					0.0215	0.0773 0.0781		.0218	OZ.
UBABSL4_12854G0011	741 Probable conjugal transfer protein (TraD)				0.0206	0.0175			.0325 UBAL3_69480060	35
UBABSL4_12854G0012	467 Putative conjugal transfer protein (TraA)				0.0200	0.0711	0.2376 0.3549 0.1344		.0211 UBAL3_69480059	59
UBABSL4_12854G0013	81 IstB domain protein ATP-binding protein				5.0771 0.4956 0.9249 0.7478 1.6669 1.9784		5.48 7.6722 4.1468		.0364 UBAL3_80630092	99
UBABSL4_12854G0014	470 Putative conjugal transfer protein (TraA)					0.0153			.0279 UBAL3_69480059	45
UBABSL4_12854G0015	22 hypothetical protein									
UBABSL4_11026G0001	143 phosphoribosylformylglycinamidine cyclo-ligase					0.0807			UBAL3_92050044	86
UBABSL4 11026G0002	340 Conserved hypothetical protein					0.0212			UBAL3_92050043	42
UBABSL4 11026G0004	382 Conserved hypothetical protein					0.102			UBAL3_92050042	76
UBABSL4_11026G0005	170 Ribonuclease III					0.0339			UBAL3_92050041	82
UBABSL4_11026G0006	229 3-oxoacyl-(Acyl-carrier-protein) synthase II (EC 2.3.1	.41)		0.02371		0.0189			UBAL3_92050040	85
UBABSL4_11026G0007	166 3-oxoacyl-(Acyl-carrier-protein) synthase II (EC 2.3.1.4					0.1043			UBAL3_92050040	88
UBABSL4_11026G0008	77 acyl carrier protein		0.14014	0.35252		0.1124			UBAL3_92050039	97
UBABSL4_11026G0009	255 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.	100)		0.00852		0.0735			UBAL3_92050038	83
UBABSL4_11026G0010	312 malonyl CoA-acyl carrier protein transacylase			0.03132		0.0046			UBAL3_92050037	65
UBABSL4_11026G0011	331 3-oxoacyl-(acyl-carrier-protein) synthase III		0.01087	0.0164		0.0305			UBAL3_92050036	82
UBABSL4_11026G0012	336 fatty acid/phospholipid synthesis protein PlsX			0.00646		0.0215			UBAL3_92050035	69
UBABSL4_11026G0013	61 Ribosomal protein S32					0.0236			UBAL3_92050034a	90
UBABSL4_11026G0014	162 Conserved protein of unknown function			0.14745		0.0445			UBAL3_92050034	65
UBABSL4_11026G0015	165 prolyl-tRNA synthetase					0.0175			UBAL3_92050033	74
UBABSL4_11196G0001	81 Conserved protein of unknown function					0.0178			UBAL3_80630032	74
UBABSL4_11196G0002	287 flagellin domain protein	0.80174	0.08146	0.10971		0.0503			UBAL3_80630031	94
UBABSL4_11196G0003	115 Probable anti-sigma-28 factor, FlgM					0.2133			UBAL3_80630030	61
UBABSL4_11196G0004	154 Conserved hypothetical protein					0.0562			UBAL3_80630029	63
UBABSL4_11196G0005	309 <mark>flagellar hook-associated protein FlgK</mark>	0.13141	0.03492	0.00703		0.056			UBAL3_80630028	72
UBABSL4_11196G0006	209 flagellar hook-associated protein FlgK					0.0414			UBAL3_80630028	72
UBABSL4_11196G0007	313 Probable flagellar hook-associated protein, FlgL	0.45406	0.02873	0.03122		0.0876			UBAL3_80630027	86
UBABSL4_11196G0008	50 hypothetical protein								UD A LO CO (COCC)	/ 7
UBABSL4_11196G0009	95 Conserved protein of unknown function	00 0001	1.02.402	1 27 400		0.7500			UBAL3_80630026	67
UBABSL4_11196G0010 UBABSL4_11196G0012	199 flagellin domain protein	20.9831	1.93403	0.00448		0.7599 0.0327			UBAL3_80630025	84
UBABSL4_11196G0012	485 Putative flagellar hook-associated protein, FliD 87 flagellar protein FliS			0.00446		0.0327			UBAL3_80630024 UBAL3_80630023	70
UBABSL4_11196G0014	129 Conserved hypothetical protein					0.0477			UBAL3_80630023 UBAL3_80630022	48
UBABSL4_11196G0015	119 Conserved protein of unknown function					0.0485			UBAL3_80630021	64
05/15021_1117000010	The Conserved protein of Granto Million Conserved					0.0 100			05/120_0000021	
UBABSL4_11888G0001	25 hypothetical protein									
UBABSL4_11888G0002	146 Conserved hypothetical protein									
UBABSL4_11888G0003	329 ABC transporter, periplasmic component		0.09293	0.0495		0.0526			UBAL3_48660049	47
UBABSL4_11888G0004	201 Conserved protein of unknown function		0.0001:	1.0000		0.0144			UBAL3_80630096	75
UBABSL4_11888G0005	153 Putative flavohemoprotein		0.39966	1.09994		0.2546			UBAL3_80630095	85
UBABSL4_11888G0005a	71 Conserved protein of unknown function			0.00000		0.1016			UBAL3_80630085	81
UBABSL4_11888G0006	116 Conserved protein of unknown function			0.02808		0.0497 0.0118			UBAL3_80630085	77 48
UBABSL4_11888G0007 UBABSL4_11888G0008	368 glycine cleavage system T protein 133 glycine cleavage H-protein	0.10177	0.51385	0.03836		0.0118			UBAL3_80630084 UBAL3_80630083	68 75
UBABSL4_11888G0009	418 Glycine dehydrogenase (decarboxylating)	0.101//	0.51565	1.40743		0.0342			UBAL3_80630082	73 68
UBABSL4_11888G0010	105 transposase					0.055			0b/\L5_00050002	00
05.15021_1100000010	.00					5.000				

UBABSL4_11888G0011	266 transposase								0.0271				
UBABSL4_11888G0012	221 thioredoxin reductase		0.02456						0.0065			UBAL3_94530070	
UBABSL4_11888G0013	69 Conserved protein of unknown function								0.0209			UBAL3_94530069	77
UBABSL4_7945G0001	55 Conserved hypothetical protein												
UBABSL4_7945G0002	41 hypothetical protein												
UBABSL4_7945G0003	110 hypothetical protein											UD A L 2 00 1 500 40	0.5
UBABSL4_7945G0005	138 Ketosteroidisomerase-related protein							0.2514	0.0057			UBAL3_80150042	
UBABSL4_7945G0006	255 Conserved hypothetical protein							0.2314	0.0057			0.0086 UBAL3_80150043	04
UBABSL4_7945G0007 UBABSL4_7945G0008	160 hypothetical protein 67 Conserved hypothetical protein (TN)												
UBABSL4_7945G0009	58 hypothetical protein												
UBABSL4_7945G0010	64 hypothetical protein												
UBABSL4_7945G0011	325 Putative conjugal transfer protein (TraA)											UBAL3 69480059	47
UBABSL4_7945G0012	371 Ti-type conjugative transfer relaxase TraA											05/120_0/ 10000/	
UBABSL4_7945G0013	223 Conserved hypothetical protein												
UBABSL4_7945G0014	126 Conserved hypothetical protein											UBAL3_96270025	32
UBABSL4_10737G0001	112 hypothetical protein			1.6319 5.7351					0.1932		0.0925		
UBABSL4_10737G0002	192 transposase			2.0626 4.391	15.023	12.935	13.362	0.5842			0.0539		
UBABSL4_10737G0003	50 transposase									1.2105			
tRNA-Leu-TAG	tRNA Leu TAG											UB 410 000 500 500 500 500 500 500 500 500 5	
UBABSL4_10737G0004	286 Conserved hypothetical protein								0.0000			UBAL3_92050183	
UBABSL4_10737G0005 UBABSL4_10737G0006	933 Probable ATP-dependent Clp protease 217 excinuclease ABC. C subunit								0.0093			UBAL3_92050184	
UBABSL4_10737G0006 UBABSL4_10737G0007	317 excinuclease ABC, C subunit								0.0332			UBAL3_92050185 UBAL3_92050185	
UBABSL4 10737G0008	84 Conserved hypothetical protein											UBAL3_92050186	
UBABSL4_10737G0009	147 Cell division protein (FtsY)		0.01477						0.0098			UBAL3_92050187	
UBABSL4_10737G0010	145 Conserved protein of unknown function		0.01477						0.0070			UBAL3_92050188	
UBABSL4_10737G0011	205 Putative phosphate starvation-inducible protein (PhoH)	0.12282	0.10593						0.0141			UBAL3_92050189	
UBABSL4_10737G0012		276 1.5966	0.15511						0.8685			UBAL3_94240192	
UBABSL4_11503G0001	375 Osmosensitive K+ channel His kinase sensor											UBAL3_95450016	
UBABSL4_11503G0002	495 Probable transporter											UBAL3_78920073	
UBABSL4_11503G0003	177 Conserved hypothetical protein											UBAL3_95450063	
UBABSL4_11503G0005	281 Nitrogenase iron protein (NifH) (EC 1.18.6.1)											UBAL3_78920077	
UBABSL4_11503G0006	447 Nitrogenase, molybdenum-iron protein alpha chain (NifD) (0.0032			UBAL3_78920078	
UBABSL4_11503G0007	405 Nitrogenase, molybdenum-iron protein beta chain (NifK) (Ed.											UBAL3_78920079	
UBABSL4_11503G0009	467 Nitrogenase MoFe cofactor biosynthesis protein (NifE) (EC 1	,	10 / 11									UBAL3_78920080	
UBABSL4_11503G0010 UBABSL4_11503G0011	478 Nitrogenase molybdenum-iron cofactor biosynthesis proteir 133 Nitrogenase molybdenum-iron protein (NifX)	I (INIIIN) (EC I.	10.6.1)									UBAL3_78920081 UBAL3_78920082	80 86
UBABSL4_11503G0011	154 NifX-associated protein											UBAL3_78920083	
UBABSL4_11503G0013	522 Nitrogenase cofactor biosynthesis protein (NifB)											UBAL3_78920085	
UBABSL4_11503G0014	86 Putative ferredoxin											UBAL3_78920086	
UBABSL4_11503G0015	23 hypothetical protein												
	·												
UBABSL4_11887G0001	288 Signal transduction histidine kinase								0.0801				
UBABSL4_11887G0002	371 Conserved hypothetical protein								0.1167				
UBABSL4_11887G0003	60 hypothetical protein												
UBABSL4_11887G0004	93 HNH endonuclease											UBAL3_48660076	
UBABSL4_11887G0005	449 Probable transport protein								0.0171			UBAL3_80290078	
UBABSL4_11887G0006 UBABSL4_11887G0007	169 DNA-3-methyladenine glycosylase (EC 3.2.2.21) 441 Phosphoketolase (EC 4.1.2.9)	0.04494	0.03939			0 1274	0.1531	0.0242	0.0171	0.20	085 0.3053 0.2136 0.1358	UBAL3_80290080 0.119 UBAL3_80290081	63 87
UBABSL4_11887G0008	232 Phosphoketolase (EC 4.1.2.7)	0.04400	0.03737			0.13/4	0.1551	0.0303	0.0435	0.20	000 0.0000 0.2100 0.1000	UBAL3_80290081	87
UBABSL4_11887G0010	201 hypothetical protein								0.0400			0B/\L3_002/0001	07
UBABSL4_11887G0011	467 Multi-sensor signal transduction histidine kinase		0.01395						0.0278			UBAL3_80290082	68
UBABSL4_11887G0012	395 Diguanylate cyclase/phosphodiesterase with PAS/PAC sens	or(s)							0.0183			UBAL3_80290084	
UBABSL4_11887G0013	85 Glycogen synthase (EC 2.4.1.21)	1.7										UBAL3_80290085	
UBABSL4_11887G0014	96 Glycogen synthase (EC 2.4.1.21)											UBAL3_80290085	
UBABSL4_12165G0001	114 Conserved hypothetical protein											UBAL3_92050124	
UBABSL4_12165G0002	219 ferredoxin								0.0395			UBAL3_92050125	
UBABSL4_12165G0003	Putative fumarate reductase/succinate dehydrogenc 0.03								0.0451			UBAL3_92050126	
UBABSL4_12165G0004	396 succinyl-CoA synthetase, beta subunit 0.5	127 1.04457	0./2109						0.0364			UBAL3_92050127	89

UBABSL4 12165G0	307 succinyl-CoA synthetase, alpha subunit	0.11022 0.48037 0.31122	0.1034	UBAL3_92050128 94
UBABSL4_12165G0		0.43106 0.80187 0.57399	0.1195	UBAL3_92050129 93
	·	0.43100 0.00107 0.37377	0.1173	0BAL3_72030127 73
UBABSL4_12165G0				
UBABSL4_12165G0				
UBABSL4_12165G0	336 NADH dehydrogenase (Quinone)		0.0301	UBAL3_94240063 73
UBABSL4_12165G0	155 Conserved hypothetical protein		0.0093	
UBABSL4_12165G0	0011 523 Conserved hypothetical protein	0.01038	0.0221	
UBABSL4_12165G0	74 hypothetical protein			
UBABSL4_12165G0	285 Conserved protein of unknown function		0.0101	UBAL3_94240065 64
UBABSL4_1756G00	140 Peptidoglycan glycosyltransferase (EC 2.4.1.129)		0.0206	UBAL3_94530108 83
UBABSL4 1756G00			0.0200	UBAL3_94530109 69
UBABSL4_1756G00	**		0.0534	UBAL3_94530110 82
UBABSL4_1756G00			0.0068	UBAL3_96270001 59
UBABSL4_1756G00	to the second se			UBAL3_96270002 58
UBABSL4_1756G00			0.0089	UBAL3_96270002 80
UBABSL4_1756G00	i e		0.0066	UBAL3_94240001 67
UBABSL4_1756G00			0.0119	UBAL3_94240002 51
UBABSL4_1756G00	396 DNA uptake lipoprotein		0.0291	UBAL3_94240004 92
UBABSL4_1756G00	134 hypothetical protein		0.0646	
UBABSL4_1756G00	74 hypothetical protein			
UBABSL4_1756G00	172 two component, sigma54 specific, transcriptional re	gulator, Fis family	0.0252	UBAL3_94240006 59
UBABSL4_3335G00	198 acriflavin resistance protein		0.0073	UBAL3_92050088 91
UBABSL4_3335G00	73 Conserved protein of unknown function		0.0198	UBAL3_92050089 72
UBABSL4 3335G00				UBAL3_92050090 76
UBABSL4_3335G00	, , , , , , , , , , , , , , , , , , , ,		0.0208	UBAL3_92050090 82
UBABSL4_3335G00			0.7768	UBAL3_92050091 64
UBABSL4_3335G00			0.7700	UBAL3_92050092 70
UBABSL4_3335G00				UBAL3_92050092 84
		0.23206	1.2565	UBAL3_72030072 64
UBABSL4_3335G00		0.23206	1.2363	
UBABSL4_3335G00	· · · · · · · · · · · · · · · · · · ·		0.0100	UD 410 00050000 57
UBABSL4_3335G00	· ·		0.0108	UBAL3_92050093 56
UBABSL4_3335G00		1.30236 0.41408 0.22013	0.0545	UBAL3_92050094 90
UBABSL4_3335G00	85 XRE family plasmid maintenance system antidote pr	otein		
UBABSL4_3478G00	· ·			UBAL3_80420040 36
UBABSL4_3478G00	· · · · · · · · · · · · · · · · · · ·		0.0059	UBAL3_80420039 42
UBABSL4_3478G00				UBAL3_80420039 62
UBABSL4_3478G00	262 penicillin-binding protein, transpeptidase		0.0496	UBAL3_80420038 78
UBABSL4_3478G00	147 Conserved protein of unknown function			UBAL3_80420036 80
UBABSL4_3478G00	138 Ribosomal protein L17	1.22602 2.46312 2.87959	0.0627	UBAL3_80420035 91
UBABSL4_3478G00	OOS 331 DNA-directed RNA polymerase, alpha subunit	0.1793 0.46579		UBAL3_80420034 75
UBABSL4_3478G00	210 Ribosomal protein S4	0.3545 0.36826 0.37743		UBAL3_80420033 85
UBABSL4_3478G00	006a 129 Ribosomal protein S11	0.27883 0.12625		UBAL3_80420032 95
UBABSL4_3478G00	007a 125 Ribosomal protein \$13	0.05755 0.15635		UBAL3_80420031 83
UBABSL4_3478G00				
	38 translation initiation factor IF-1			UBAL3 80420029 100
		0.00965	0.0064	UBAL3_80420029 100 UBAL3_80420028 71
UBABSL4_3478G00		0.00965	0.0064	UBAL3_80420029 100 UBAL3_80420028 71
UBABSL4_3478G00	225 methionine aminopeptidase, type I		0.0064 0.0526	UBAL3_80420028 71
UBABSL4_3478G00	225 methionine aminopeptidase, type I 247 Glucosamine-1-phosphate n-acetyltransferase] (EC		0.0526	UBAL3_80420028 71 UBAL3_74420044 57
UBABSL4_3478G00 UBABSL4_5705G00 UBABSL4_5705G00	methionine aminopeptidase, type I 247 Glucosamine-1-phosphate n-acetyltransferase] (EC 41 Conserved protein of unknown function	2.3.1.157)	0.0526 0.0352	UBAL3_80420028 71 UBAL3_74420044 57 UBAL3_74420045 78
UBABSL4_3478G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00	methionine aminopeptidase, type I 247 Glucosamine-1-phosphate n-acetyltransferase] (EC 41 Conserved protein of unknown function 122 Conserved protein of unknown function		0.0526 0.0352 0.0828	UBAL3_80420028 71 UBAL3_74420044 57 UBAL3_74420045 78 UBAL3_74420046 47
UBABSL4_3478G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00	methionine aminopeptidase, type I 247 Glucosamine-1-phosphate n-acetyltransferase] (EC 41 Conserved protein of unknown function 122 Conserved protein of unknown function 227 Conserved protein of unknown function	2.3.1.157)	0.0526 0.0352 0.0828 0.0254	UBAL3_80420028 71 UBAL3_74420044 57 UBAL3_74420045 78 UBAL3_74420046 47 UBAL3_74420047
UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00	methionine aminopeptidase, type I 247 Glucosamine-1-phosphate n-acetyltransferase] (EC 41 Conserved protein of unknown function 122 Conserved protein of unknown function 227 Conserved protein of unknown function 153 Conserved protein of unknown function	2.3.1.157)	0.0526 0.0352 0.0828	UBAL3_80420028 71 UBAL3_74420044 57 UBAL3_74420045 78 UBAL3_74420047 47 UBAL3_74420047 74
UBABSL4_3478G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00	methionine aminopeptidase, type I 247 Glucosamine-1-phosphate n-acetyltransferase] (EC 41 Conserved protein of unknown function 122 Conserved protein of unknown function 227 Conserved protein of unknown function 153 Conserved protein of unknown function 122 Putative LD-carboxypeptidase family protein	2.3.1.157)	0.0526 0.0352 0.0828 0.0254	UBAL3_80420028 71 UBAL3_74420044 57 UBAL3_74420045 78 UBAL3_74420046 47 UBAL3_74420047 74 UBAL3_74420047 74 UBAL3_74420048 60
UBABSL4_3478G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00	methionine aminopeptidase, type I 247 Glucosamine-1-phosphate n-acetyltransferase] (EC 41 Conserved protein of unknown function 122 Conserved protein of unknown function 227 Conserved protein of unknown function 153 Conserved protein of unknown function 122 Putative LD-carboxypeptidase family protein 147 Putative LD-carboxypeptidase family protein	2.3.1.157)	0.0526 0.0352 0.0828 0.0254	UBAL3_80420028 71 UBAL3_74420044 57 UBAL3_74420045 78 UBAL3_74420046 47 UBAL3_74420047 74 UBAL3_74420047 74 UBAL3_74420048 60 UBAL3_74420048 60
UBABSL4_3478G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00 UBABSL4_5705G00	methionine aminopeptidase, type I 247 Glucosamine-1-phosphate n-acetyltransferase] (EC 41 Conserved protein of unknown function 122 Conserved protein of unknown function 123 Conserved protein of unknown function 124 Conserved protein of unknown function 125 Conserved protein of unknown function 126 Undata Putative LD-carboxypeptidase family protein 127 Putative LD-carboxypeptidase family protein 128 Conserved hypothetical protein 129 Roman State Putative LD-carboxypeptidase family protein 147 Putative LD-carboxypeptidase family protein	2.3.1.157)	0.0526 0.0352 0.0828 0.0254 0.0566	UBAL3_80420028 71 UBAL3_74420044 57 UBAL3_74420045 78 UBAL3_74420047 UBAL3_74420047 UBAL3_74420047 74 UBAL3_74420048 60 UBAL3_74420048 60 UBAL3_74420049 54
UBABSL4_5705G00	methionine aminopeptidase, type I 247 Glucosamine-1-phosphate n-acetyltransferase] [EC 41 Conserved protein of unknown function 122 Conserved protein of unknown function 227 Conserved protein of unknown function 153 Conserved protein of unknown function 152 Putative LD-carboxypeptidase family protein 147 Putative LD-carboxypeptidase family protein 181 Conserved hypothetical protein 185 Cobyrinic acid a,c-diamide synthase	2.3.1.157)	0.0526 0.0352 0.0828 0.0254 0.0566	UBAL3_80420028 71 UBAL3_74420044 57 UBAL3_74420045 78 UBAL3_74420047 47 UBAL3_74420047 74 UBAL3_74420048 60 UBAL3_74420048 60 UBAL3_74420049 54 UBAL3_74420050 82
UBABSL4_5705G00	methionine aminopeptidase, type I 247 Glucosamine-1-phosphate n-acetyltransferase] (EC 41 Conserved protein of unknown function 122 Conserved protein of unknown function 227 Conserved protein of unknown function 153 Conserved protein of unknown function 152 Putative LD-carboxypeptidase family protein 147 Putative LD-carboxypeptidase family protein 147 Conserved hypothetical protein 185 Cobyrinic acid a,c-diamide synthase 136 Creatininase	2.3.1.157)	0.0526 0.0352 0.0828 0.0254 0.0566	UBAL3_80420028 71 UBAL3_74420044 57 UBAL3_74420045 78 UBAL3_74420046 47 UBAL3_74420047 74 UBAL3_74420048 60 UBAL3_74420048 60 UBAL3_74420049 54 UBAL3_74420050 82 UBAL3_74420051 81
UBABSL4_5705G00	methionine aminopeptidase, type I 247 Glucosamine-1-phosphate n-acetyltransferase] (EC 41 Conserved protein of unknown function 227 Conserved protein of unknown function 227 Conserved protein of unknown function 153 Conserved protein of unknown function 122 Putative LD-carboxypeptidase family protein 147 Putative LD-carboxypeptidase family protein 147 Putative LD-carboxypeptidase family protein 155 Conserved hypothetical protein 160 Conserved hypothetical protein 170 Conserved hypothetical protein	2.3.1.157) 0.11094 0.0178	0.0526 0.0352 0.0828 0.0254 0.0566	UBAL3_80420028 71 UBAL3_74420044 57 UBAL3_74420045 78 UBAL3_74420047 UBAL3_74420047 74 UBAL3_74420048 60 UBAL3_74420048 60 UBAL3_74420049 54 UBAL3_74420050 82 UBAL3_74420051 81 UBAL3_95450144 69
UBABSL4_5705G00	methionine aminopeptidase, type I 247 Glucosamine-1-phosphate n-acetyltransferase] (EC 41 Conserved protein of unknown function 227 Conserved protein of unknown function 227 Conserved protein of unknown function 153 Conserved protein of unknown function 122 Putative LD-carboxypeptidase family protein 147 Putative LD-carboxypeptidase family protein 147 Putative LD-carboxypeptidase family protein 155 Conserved hypothetical protein 160 Conserved hypothetical protein 170 Conserved hypothetical protein	2.3.1.157) 0.11094 0.0178	0.0526 0.0352 0.0828 0.0254 0.0566	UBAL3_80420028 71 UBAL3_74420044 57 UBAL3_74420045 78 UBAL3_74420046 47 UBAL3_74420047 74 UBAL3_74420048 60 UBAL3_74420048 60 UBAL3_74420049 54 UBAL3_74420050 82 UBAL3_74420051 81
UBABSL4_5705G00	225 methionine aminopeptidase, type I 247 Glucosamine-1-phosphate n-acetyltransferase] (EC 41 Conserved protein of unknown function 122 Conserved protein of unknown function 123 Conserved protein of unknown function 124 Conserved protein of unknown function 125 Conserved protein of unknown function 126 Putative LD-carboxypeptidase family protein 127 Putative LD-carboxypeptidase family protein 128 Conserved hypothetical protein 129 Romanus Conserved protein 120 Creatininase 120 diguanylate cyclase/phosphodiesterase 40 Putative CO dehydrogenase beta subunit/acetyl-C	2.3.1.157) 0.11094 0.0178	0.0526 0.0352 0.0828 0.0254 0.0566	UBAL3_80420028 71 UBAL3_74420044 57 UBAL3_74420045 78 UBAL3_74420047 UBAL3_74420047 74 UBAL3_74420048 60 UBAL3_74420048 60 UBAL3_74420049 54 UBAL3_74420050 82 UBAL3_74420051 81 UBAL3_95450144 69
UBABSL4_5705G00	225 methionine aminopeptidase, type I 247 Glucosamine-1-phosphate n-acetyltransferase] [EC 41 Conserved protein of unknown function 222 Conserved protein of unknown function 225 Conserved protein of unknown function 226 Conserved protein of unknown function 227 Conserved protein of unknown function 228 Putative LD-carboxypeptidase family protein 229 Putative LD-carboxypeptidase family protein 230 Conserved hypothetical protein 240 Conserved hypothetical protein 250 Copyrinic acid a,c-diamide synthase 260 Creatininase 270 Putative CO dehydrogenase beta subunit/acetyl-C	2.3.1.157) 0.11094 0.0178 DA synthase epsilon subunit	0.0526 0.0352 0.0828 0.0254 0.0566	UBAL3_80420028 71 UBAL3_74420044 57 UBAL3_74420045 78 UBAL3_74420047 4 UBAL3_74420047 74 UBAL3_74420048 60 UBAL3_74420049 54 UBAL3_74420050 82 UBAL3_74420051 81 UBAL3_74420055 90
UBABSL4_5705G00	225 methionine aminopeptidase, type I 247 Glucosamine-1-phosphate n-acetyltransferase] [EC 41 Conserved protein of unknown function 222 Conserved protein of unknown function 225 Conserved protein of unknown function 226 Conserved protein of unknown function 227 Conserved protein of unknown function 228 Putative LD-carboxypeptidase family protein 229 Putative LD-carboxypeptidase family protein 230 Conserved hypothetical protein 240 Conserved hypothetical protein 250 Copyrinic acid a,c-diamide synthase 260 Creatininase 270 Putative CO dehydrogenase beta subunit/acetyl-C	2.3.1.157) 0.11094 0.0178 DA synthase epsilon subunit	0.0526 0.0352 0.0828 0.0254 0.0566	UBAL3_80420028 71 UBAL3_74420044 57 UBAL3_74420045 78 UBAL3_74420047 UBAL3_74420047 74 UBAL3_74420048 60 UBAL3_74420048 60 UBAL3_74420049 54 UBAL3_74420050 82 UBAL3_74420051 81 UBAL3_95450144 69

UBABSL4_11740G0	214 Conserved protein of unknown function		0.0472	UBAL3_95680018	63
UBABSL4_11740G0	166 Conserved hypothetical protein			UBAL3_95680019	42
UBABSL4_11740G0	0005 457 putative adenylate/guanylate cyclase			UBAL3_95680020	53
UBABSL4_11740G0	0006 486 Conserved hypothetical protein		0.0119	UBAL3_95680021	49
UBABSL4_11740G0	309 Conserved protein of unknown function		0.0187	UBAL3_95680022	44
UBABSL4_11740G0	80 Putative ABC transporter				59
UBABSL4_11740G0					82
UBABSL4_11740G0	· ·		0.0192		53
UBABSL4_11740G0			0.0068		81
UBABSL4_11740G0	89 Cytochrome-c peroxidase			UBAL3_95680026	70
UBABSL4_11853G0	0001 402 UDP-N-acetylglucosamine 1-carboxyvinyltransferas	e 0.00895 0.0108	0.0072	UBAL3_94240186	77
UBABSL4_11853G0		0.01501	0.0133		71
UBABSL4_11853G0		0.04657 0.0825 0.1021	0.0066		69
UBABSL4_11853G0			0.0199		49
UBABSL4_11853G0					75
UBABSL4_11853G0	69 imidazole glycerol phosphate synthase, glutamine		0.0209	UBAL3_94240181	71
UBABSL4_11853G0	120 imidazole glycerol phosphate synthase, glutamine		0.0361	UBAL3_94240181	74
UBABSL4_11853G0	250 phosphoribosylformimino-5-aminoimidazole	0.02606	0.0231		68
UBABSL4_11853G0		0.19741	0.0164		89
UBABSL4_11853G0			0.0286		69
UBABSL4_11853G0	, , , :	0.07005			66
UBABSL4_11853G0	31 Ribosomal protein S21	0.07005	0.2327	UBAL3_94240176 1	100
UBABSL4_11894G0	245 Putative methyltransferase		0.0177	UBAL3 80630020	65
UBABSL4_11894G0	The state of the s		0.0027		51
UBABSL4_11894G0	1 7 7 7 1 7 1		0.0194		63
UBABSL4_11894G0			0.0341		71
UBABSL4_11894G0	0005 449 Probable heptosyltransferase family protein		0.0096	UBAL3_80630017	71
UBABSL4_11894G0	174 Probable heptosyltransferase family protein			UBAL3_80630017	55
UBABSL4_11894G0	228 Conserved protein of unknown function			UBAL3_80630016	57
UBABSL4_11894G0					
UBABSL4_11894G0			0.0497		58
UBABSL4_11894G0			0.0215		81
UBABSL4_11894G0	The state of the s		0.143	UBAL3_80630010	86
UBABSL4_11894G0	134 hypothetical protein				
UBABSL4_4178G00	119 oxidoreductase FAD/NAD(P)-binding domain		0.0485	UBAL3_69480044	36
UBABSL4_4178G00	95 oxidoreductase FAD/NAD(P)-binding domain			UBAL3_69480044	
UBABSL4_4178G00	552 diguanylate cyclase/phosphodiesterase with GAF		0.0052	UBAL3_69480045	32
UBABSL4_4178G00	117 hypothetical protein				
UBABSL4_4178G00					
UBABSL4_4178G00	The state of the s		0.0099		
UBABSL4_4178G00		0.0000	0.004		
UBABSL4_4178G00	The state of the s	0.00983	0.0326	110 41 3 70 4000 43	15
UBABSL4_4178G00 UBABSL4_4178G00	· ·		0.0055 0.0025		65 86
UBABSL4_4178G00	~ ~		0.0023		60
05/15024_41/0000	277 Honoxygonaso, 1712 Sinding			OB/120_0/400041	00
UBABSL4_7770G00	341 Nitrite/sulfite reductase		0.0465	UBAL3_95680100	57
UBABSL4_7770G00	136 Conserved protein of unknown function			UBAL3_95680099	46
UBABSL4_7770G00					
UBABSL4_7770G00	795 hypothetical protein	0.00956	0.0036	0.0014	
UBABSL4_7770G00			0.0294	UBAL3_80420059	
UBABSL4_7770G00				UBAL3_80420057	
UBABSL4_7770G00	· · · · · · · · · · · · · · · · · · ·	0.11700	0.0401		32
UBABSL4_7770G00		0.11738	0.0439	UBAL3_80420058	41
UBABSL4_7770G00 UBABSL4_7770G00		0.07403	0.0164	UBAL3_79320011	41
UBABSL4_7770G00					
32/13024_///0000	2.5 marrier made by Grant protontile				
UBABSL4_9876G00	349 flagellar M-ring protein FliF		0.0289	UBAL3_80630068	82
UBABSL4_9876G00	· · · · · · · · · · · · · · · · · · ·		0.0108		98
UBABSL4_9876G00	106 Flagellar hook-basal body complex subunit FliE		0.0408	UBAL3_80630069	91

UBABSL4_9876G0003 UBABSL4_9876G0004 UBABSL4_9876G0005 UBABSL4_9876G0006 UBABSL4_9876G0007 UBABSL4_9876G0008 UBABSL4_9876G0009 UBABSL4_9876G0010	146 flagellar basal-body rod protein FIgC 125 flagellar basal-body rod protein FIgB 460 Putative two component, sigma54 specific, transcripti 251 Putative PAS/PAC sensor signal transduction histidine F 77 Putative PAS/PAC sensor signal transduction histidine F 544 Putative TPR-domain containing protein 280 sigma54 specific transcriptional regulator, Fis family 77 sigma54 specific transcriptional regulator, Fis family	kinase	0.0692 0.0115 0.0314 0.0287 0.0187 0.0186 0.0361 0.0375		UBAL3_80630070 87 UBAL3_80630071 90 UBAL3_80630072 79 UBAL3_80630073 60 UBAL3_80630073 50 UBAL3_80630074 55 UBAL3_80630076 66 UBAL3_80630076 70
UBABSL4_10765G0001 UBABSL4_10765G0002 UBABSL4_10765G0003 UBABSL4_10765G0004 UBABSL4_10765G0005 UBABSL4_10765G0006 UBABSL4_10765G0007 UBABSL4_10765G0007	420 Alpha,alpha-trehalose-phosphate synthase 272 Trehalose-6-phosphate phosphatase 302 dTDP-4-dehydrorhamnose reductase 225 ADP-L-glycero-D-manno-heptose-6-epimerase 613 Conserved protein of unknown function 117 cytochrome c, class I 90 Conserved hypothetical protein 125 Conserved hypothetical protein	0.0193	0.0481 0.0106 0.0382 0.109 0.0094 0.0123		UBAL3_95450128 60 UBAL3_95450127 54 UBAL3_95450126 60 UBAL3_95450123 77 UBAL3_95450122 64 UBAL3_95450121 47
UBABSL4_10765G0009 UBABSL4_10765G0010 UBABSL4_10765G0011	121 Conserved hypothetical protein 586 transposase 110 Conserved hypothetical protein	0.00741	0.0131		
UBABSL4_11442G0001 UBABSL4_11442G0002 UBABSL4_11442G0003 UBABSL4_11442G0004 UBABSL4_11442G0005 UBABSL4_11442G0006	94 Putative pirin domain protein 69 Conserved protein of unknown function 71 Conserved protein of unknown function 376 Putative sulfide-quinone reductase 63 hypothetical protein 392 Conserved hypothetical protein		0.0614 0.1254 0.1422 0.0192		UBAL3_80290032 85 UBAL3_80290033 66 UBAL3_80290033 58 UBAL3_80290034 67 UBAL3_80290036 37
UBABSL4_11442G0007 UBABSL4_11442G0008 UBABSL4_11442G0009 UBABSL4_11442G0010 UBABSL4_11442G0011	146 Conserved hypothetical protein 60 hypothetical protein 639 Probable citrate transporter 275 Conserved protein of unknown function 148 Putative transcriptional regulator, MarR family		0.024 0.0113 0.0052 0.0097		UBAL3_80290038 64 UBAL3_80290039 53 UBAL3_80290040 78
UBABSL4_11480G0001 UBABSL4_11480G0002	274 Putative glycosyl hydrolase, BNR repeat 215 Conserved protein of unknown function	0.01313	0.2211 0.1275	0.0189	UBAL3_92050057 83 UBAL3_92050058 75
UBABSL4_11480G0003 UBABSL4_11480G0004 UBABSL4_11480G0005 UBABSL4_11480G0006 UBABSL4_11480G0007	119 Conserved protein of unknown function 86 Conserved protein of unknown function 89 Conserved hypothetical protein 308 Putative oligopeptide ABC transporter 96 Putative oligopeptide ABC transporter				UBAL3_92050059 52 UBAL3_92050060 56 UBAL3_92050061 58 UBAL3_92050062 85 UBAL3_92050063 88
UBABSL4_11480G0004 UBABSL4_11480G0005 UBABSL4_11480G0006	86 Conserved protein of unknown function 89 Conserved hypothetical protein	0.06661	0.0509 0.0266 0.0024 0.156		UBAL3_92050060 56 UBAL3_92050061 58 UBAL3_92050062 85
UBABSL4_11480G0004 UBABSL4_11480G0005 UBABSL4_11480G0006 UBABSL4_11480G0008 UBABSL4_11480G0009 UBABSL4_11480G0010 UBABSL4_11480G0011 UBABSL4_112275G0001 UBABSL4_12275G0002 UBABSL4_12275G0005 UBABSL4_12275G0007	86 Conserved protein of unknown function 89 Conserved hypothetical protein 308 Putative oligopeptide ABC transporter 96 Putative oligopeptide ABC transporter 85 Putative oligopeptide ABC transporter 326 Conserved protein of unknown function 609 Conserved hypothetical protein 111 transposase 86 hypothetical protein 503 RNA-directed DNA polymerase 460 Putative endonuclease 204 Arsenical resistance operon trans-acting	0.06661	0.0266 0.0024		UBAL3_92050060 56 UBAL3_92050061 58 UBAL3_92050062 85 UBAL3_92050063 88 UBAL3_92050064 52 UBAL3_945300060 67 UBAL3_945300061 65 UBAL3_94530056 76 UBAL3_94530056 76 UBAL3_95450074 53
UBABSL4_11480G0004 UBABSL4_11480G0005 UBABSL4_11480G0006 UBABSL4_11480G0007 UBABSL4_11480G0009 UBABSL4_11480G0009 UBABSL4_11480G0010 UBABSL4_11480G0011 UBABSL4_12275G0001 UBABSL4_12275G0002 UBABSL4_12275G0002	86 Conserved protein of unknown function 89 Conserved hypothetical protein 308 Putative oligopeptide ABC transporter 96 Putative oligopeptide ABC transporter 85 Putative oligopeptide ABC transporter 326 Conserved protein of unknown function 609 Conserved hypothetical protein 111 transposase 86 hypothetical protein 503 RNA-directed DNA polymerase 460 Putative endonuclease		0.0266 0.0024 0.156		UBAL3_92050060 56 UBAL3_92050061 58 UBAL3_92050062 85 UBAL3_92050063 88 UBAL3_92050064 52 UBAL3_94530006a 67 UBAL3_945300065 65 UBAL3_94530056 76

UBABSL4_12515G0008 UBABSL4_12515G0009 UBABSL4_12515G0010 UBABSL4_12515G0011	 473 DNA repair protein RadA 289 pantoatebeta-alanine ligase 281 Putative tetrapyrrole methylase family protein 67 Probable SirA family protein 		0.00459							0.0213 0.01 0.0051 0.0215						UB.	AL3_92050020 AL3_92050019 AL3_92050018 AL3_92050017	6	35 31 32 36
UBABSL4_12832G0001 UBABSL4_12832G0002 UBABSL4_12832G0003 UBABSL4_12832G0004 UBABSL4_12832G0005 UBABSL4_12832G0006 UBABSL4_12832G0007	43 hypothetical protein 192 Conserved hypothetical protein 155 DNA (cytosine-5-)-methyltransferase 247 DNA (cytosine-5-)-methyltransferase 180 hypothetical protein 91 hypothetical protein 144 putative transcriptional regulator, MerR family			0.3542 3.6492 1.474 1.3566		0.7804 0.2417 0.3033	1.8929	2.1778	0.0649	0.3444 0.6483 0.0401		0.3887 0.7959	0.7685 0.5032	0.1215 0.3431 0.1395	1.1264	1.1636 UB 1.7436 UB 0.0243	AL3_96120003 AL3_93200035 AL3_93200035 AL3_93200020	8 7	99 34 79
UBABSL4_12832G0008 UBABSL4_12832G0009 UBABSL4_12832G0010 UBABSL4_12832G0011	131 Mercury transporter MerC 551 mercuric reductase 380 transposase, IS204/IS1001/IS1096/IS1165 family 176 Conserved protein of unknown function		0.00394	0.0829 0.0401 0.1731			0.1594			0.0551 0.0314 0.0987 0.041		0.1452 0.1093 0.1252 0.0901		0.1487	0.0676	0.0173 UB	AL3_93200019 AL3_95450062 AL3_95530042	7	19 78 60
UBABSL4_8928G0001 UBABSL4_8928G0002 UBABSL4_8928G0003 UBABSL4_8928G0004 UBABSL4_8928G0005 UBABSL4_8928G0006 UBABSL4_8928G0007 UBABSL4_8928G0008 UBABSL4_8928G0009 UBABSL4_8928G0009 UBABSL4_8928G0010	109 glucose-1-phosphate thymidylytransferase 181 dTDP-4-dehydrorhamnose 3,5-epimerase 61 hypothetical protein 200 Conserved hypothetical protein 145 transposase 455 hypothetical protein 338 cation diffusion facilitator family transporter 44 Conserved hypothetical protein 213 hypothetical protein 172 diayanylate cyclase with PAS/PAC sensor	0.1485	0.01992 0.06598	0.5891 0.2497 0.4569 2.5038 3.4145	0.6176 0.2375	0.4117 0.2217	1.1982	0.746 0.3376 0.9248 1.7805 0.1997 1.9017	3.8416	0.2391 0.1226 0.4348 0.4122 0.0939 0.5574 0.7721	0.133	0.6306 0.9876 0.4756 6.8841 6.7175 1.8667 1.8015 2.1435	0.6008 0.3396 0.5179 5.4625 5.1446 1.3789 1.177 2.2611	0.3989 0.6175 0.5023 8.1275 7.2236 1.5603 1.4982 3.1244	0.4918 0.0561 0.3423 3.5406 4.2961 1.109 0.778 3.1341	0.3261 UB, 0.1254 0.2842 UB, 2.2311 2.597 0.9928 UB, 0.4472 UB, 2.0168	AL3_94170082 AL3_94170083 AL3_94170085 AL3_93200002 AL3_93200003a AL3_93200004	10	
UBABSL4_11581G0001 UBABSL4_11581G0002 UBABSL4_11581G0003	90 Conserved hypothetical protein 81 Conserved hypothetical protein 200 Conserved hypothetical protein			0.1771				0.3923	0.0932	0.0303		0.0664	1.0536	1.1063	0.42/9	U.3493 UB/	AL3_93200004	7	3
UBABSL4_11581G0004 UBABSL4_11581G0005 UBABSL4_11581G0006 UBABSL4_11581G0007 UBABSL4_11581G0009 UBABSL4_11581G0010 UBABSL4_11581G0010 UBABSL4_11581G0011	216 TonB family protein 139 Biopolymer transport protein ExbD/TolR 140 MotA/TolG/ExbB proton channel 248 TonB-dependent receptor 373 TonB-dependent receptor 150 TonB-dependent receptor 216 two component transcriptional regulator, winged															UB, UB, UB, UB, UB,	AL3_93200026 AL3_93200025 AL3_93200024 AL3_93200033 AL3_93200033 AL3_93200033 AL3_93200028	5 6 7 8 5	18 56 53 75 37 53
UBABSL4_11758G0001 UBABSL4_11758G0002 UBABSL4_11758G0003 UBABSL4_11758G0004 UBABSL4_11758G0006 UBABSL4_11758G0007 UBABSL4_11758G0009 UBABSL4_11758G0010 UBABSL4_11758G0010 UBABSL4_11758G0011	36 hypothetical protein 309 Putative helicase 679 Putative helicase 557 Putative helicase 99 hypothetical protein 253 Conserved protein of unknown function 86 hypothetical protein 94 Single-stranded DNA-binding protein 65 hypothetical protein 143 Conserved hypothetical protein		0.01759	0.0273					0.3452	0.0207		0.0057	0.0558		0.0061	UB,	AL3_92050009 AL3_92050009 AL3_92050009 AL3_96270019 AL3_92050173 AL3_95450088	7 ¹ 6 ²	48 70 54 28 56
UBABSL4_12302G0001 UBABSL4_12302G0002	174 HNH endonuclease 110 Conserved hypothetical protein		0.01974				0.6962										AL3_48660076		75
UBABSL4_12302G0003 UBABSL4_12302G0004 UBABSL4_12302G0005 UBABSL4_12302G0006 UBABSL4_12302G0007 UBABSL4_12302G0008 UBABSL4_12302G0009	46 hypothetical protein 189 Conserved hypothetical protein 508 sigma54 specific transcriptional regulator, Fis family 367 UDP-galactopyranose mutase 73 hypothetical protein 337 glycosyl transferase, family 2 587 periplasmic sensor signal transduction histidine kinase		0.06319							0.0085 0.0342 0.0074						UB, UB, UB,	AL3_94240097 AL3_94240099 AL3_94240100 AL3_94240101	8 8 7	58 38 31 75
UBABSL4_12302G0010 UBABSL4_12310G0001 UBABSL4_12310G0002 UBABSL4_12310G0003	197 glycosyl transferase, family 282 Glycine dehydrogenase (decarboxylating)266 transposase231 Conserved protein of unknown function									0.0176 0.0163						UBA	AL3_94240102 AL3_80630081 AL3_94240165	7	70 54

UBABSL4_12310G0004 UBABSL4_12310G0005 UBABSL4_12310G0006 UBABSL4_12310G0007 UBABSL4_12310G0008	124 Conserved protein of unknown function 418 seryl-tRNA synthetase 149 Conserved protein of unknown function 119 phosphoribosyltransferase 36 hypothetical protein			0.01751 0.01558 0.01457			0.0116 0.0656		UBAL3_94240164 UBAL3_94240163 UBAL3_44810095 UBAL3_44810094	67 73 75 63
UBABSL4_12310G0009 UBABSL4_12310G0010	362 Radical SAM domain protein 223 Conserved protein of unknown function						0.0598 0.0388		UBAL3_74420056 UBAL3_74420057	70 60
UBABSL4_17878G0001 UBABSL4_17878G0002 UBABSL4_17878G0003 UBABSL4_17878G0004	206 RNA-directed DNA polymerase 227 Conserved hypothetical protein 80 hypothetical protein 85 putative GAF sensor protein						0.0191		UBAL3_93670015 UBAL3_95950035	60 4 0
UBABSL4_17878G0005 UBABSL4_17878G0006	193 hypothetical protein 92 hypothetical protein						0.0075			
UBABSL4_17878G0007 UBABSL4_17878G0008 UBABSL4_17878G0009	316 Conserved hypothetical protein 131 transposase 143 transposase						0.0091			
UBABSL4_17878G0010	53 hypothetical protein									
UBABSL4_17883G0001 UBABSL4_17883G0002 UBABSL4_17883G0003 UBABSL4_17883G0004	179 3-deoxy-manno-octulosonate-8-phosphatase 182 CDP-diacylglycerol-glycerol-3-phosphate 206 Conserved hypothetical protein 332 peptidase M23B			0.01213			0.0161		UBAL3_95950028 UBAL3_95950029 UBAL3_95950030 UBAL3_95950031	59 79 64 79
UBABSL4_17883G0005 UBABSL4_17883G0006	497 periplasmic sensor signal transduction histidine kinas	e		0.00437			0.0145		UBAL3_95950032	75
UBABSL4_17883G0007	338 Conserved hypothetical protein 243 Conserved hypothetical protein								UBAL3_95950037	59
UBABSL4_17883G0009 UBABSL4_17883G0010	153 Conserved hypothetical protein 107 Conserved hypothetical protein								UBAL3_95950038 UBAL3_95950038	55 55
UBABSL4_17883G0011	277 sodium/hydrogen exchanger								UBAL3_95950039	57
UBABSL4_3895G0001 UBABSL4_3895G0002 UBABSL4_3895G0004 UBABSL4_3895G0005 UBABSL4_3895G0006	281 methyl-accepting chemotaxis sensory transducer 203 metallo-beta-lactamase family protein 327 methyl-accepting chemotaxis sensory transducer 334 methyl-accepting chemotaxis sensory transducer 409 putative diguanylate cyclase	0.43462	0.2695	0.14277			0.0565 0.0711 0.1191 0.0734 0.1376		UBAL3_96120012 UBAL3_96120013 UBAL3_95950046 UBAL3_96120017	73 91 74 70
UBABSL4_3895G0007 UBABSL4_3895G0008	133 Conserved hypothetical protein 274 hypothetical protein				0.0556	0.2464	0.2495 0.0053			
UBABSL4_3895G0009	346 phage integrase family protein				0.088	0.2.10.1	0.0042	0.0092	UBAL3_95660014	29
UBABSL4_3895G0010	673 FOG: Transposase-like								UBAL3_94240161	46
UBABSL4_4347G0001 UBABSL4_4347G0002	200 glycoside hydrolase, family 57 117 glycoside hydrolase, family 57			0.01856			0.0617		UBAL3_94530082 UBAL3_94530082	37 60
UBABSL4_4347G0003	179 4-alpha-glucanotransferase								UBAL3_94530081	80
UBABSL4_4347G0004 UBABSL4_4347G0005	226 4-alpha-glucanotransferase 335 galactose-1-phosphate uridylyltransferase		0.20401	0.00961 0.20094			0.0447 0.0732		UBAL3_94530081 UBAL3_94530080	53 94
UBABSL4_4347G0006 UBABSL4_4347G0007	452 Probable aldolase 310 Putative glycoside hydrolase, family 57	0.26951	0.39391	0.35551			0.0128 0.0605		UBAL3_94530079 UBAL3_94530078	79 84
UBABSL4_4347G0008	50 Conserved protein of unknown function		0.14388	0.54287			0.1443		UBAL3_94530077	61
UBABSL4_4347G0009	65 hypothetical protein									
UBABSL4_4646G0001 UBABSL4_4646G0001a UBABSL4_4646G0002a	186 Putative ATP-dependent Clp protease, ATPase subuni 104 O-sialoglycoprotein endopeptidase (EC 3.4.24.57) 139 O-sialoglycoprotein endopeptidase (EC 3.4.24.57)	it	0.2514	0.32689			0.3645		UBAL3_80420043 UBAL3_80420044 UBAL3_80420044	88 73 73
UBABSL4_4646G0002	246 arginyl-tRNA synthetase						0.0469		UBAL3_80420045	61
UBABSL4_4646G0003 UBABSL4_4646G0004	179 arginyl-tRNA synthetase 190 queuine tRNA-ribosyltransferase			0.02426			0.0161		UBAL3_80420045 UBAL3_80420046	80 75
UBABSL4_4646G0005 UBABSL4_4646G0006	55 preprotein translocase, YajC subunit 211 SecD export membrane protein						0.0262		UBAL3_80420047 UBAL3_80420048	67 68
UBABSL4_4646G0006 UBABSL4_4646G0007	285 SecF export membrane protein					 	0.0962		 UBAL3_80420049	84
UBABSL4_4714G0001	77 chaperone protein DnaK		0.09343				0.2061		UBAL3_80420058	88
UBABSL4_4714G0002 UBABSL4_4714G0003	255 chaperone protein DnaK 227 heat-inducible transcription repressor HrcA	1.43315	1.76321	1.30716			0.3394 0.0064		UBAL3_80420058 UBAL3_80420055	96 66
UBABSL4_4714G0003 UBABSL4_4714G0004	96 Conserved hypothetical protein						0.0004		UBAL3_80420054	79

UBABSL4_4714G0005 UBABSL4_4714G0006 UBABSL4_4714G0007 UBABSL4_4714G0008 UBABSL4_4714G0009	303 Probable formate dehydrogenase accessory protein 756 GTP pyrophosphokinase (EC 2.7.6.5) 151 Putative RecJ exonuclease 315 Putative RecJ exonuclease 49 Conserved hypothetical protein			0.00287						0.0381 0.0191 0.0382 0.0046						U U U	BAL3_80420053 BAL3_80420052 BAL3_80420051 BAL3_80420051 BAL3_80420050	77 83 71 71 87
UBABSL4_4862G0001 UBABSL4_4862G0002 UBABSL4_4862G0003 UBABSL4_4862G0004 tRNA-Arg-TCT	207 NAD-dependent epimerase/dehydratase 169 Extradiol ring-cleavage dioxygenase, class III 71 glutaredoxin 100 Conserved hypothetical protein tRNA Arg TCT			0.03058						0.007 0.1219						U	BAL3_80630004 BAL3_80630005 BAL3_80630006 BAL3_80630006a	60 53 77 79
UBABSL4_4862G0005 UBABSL4_4862G0006 UBABSL4_4862G0007	193 carbonic anhydrase 91 Conserved hypothetical protein 56 hypothetical protein	0.14026	0.22364	0.20815						0.0598						U	BAL3_94240072	88
UBABSL4_4862G0008	325 Radical SAM superfamily protein			0.00668						0.0222						U	BAL3_94170002	88
UBABSL4_7423G0001 UBABSL4_7423G0002 UBABSL4_7423G0003 UBABSL4_7423G0004 UBABSL4_7423G0005 UBABSL4_7423G0006	197 cell division protein FtsZ 313 cell division protein FtsA 106 Conserved protein of unknown function 159 Conserved protein of unknown function 236 D-alanineD-alanine ligase 293 UDP-N-acetylmuramatealanine ligase		0.01826	0.03858 0.10407 0.06441 0.02223						0.0439 0.0323 0.0122 0.0148						U U U	BAL3_92050147 BAL3_92050146 BAL3_92050145 BAL3_92050145 BAL3_92050144 BAL3_92050142	90 73 67 47 76 73
UBABSL4_7423G0008 UBABSL4_7423G0009 UBABSL4_7423G0010	171 UDP-N-acetylmuramate-alanine ligase 279 N-acetylglucosaminyltransferase, MurG 322 Putative cell division protein (FtsW)			0.02220						0.0253						U	BAL3_92050142 BAL3_92050141 BAL3_92050140	58 76
UBABSL4_7659G0001 UBABSL4_7659G0002 UBABSL4_7659G0003 UBABSL4_7659G0004	118 Phosphoribosylglycinamide synthetase 168 Putative translation factor (SUA5) 46 Putative translation factor (SUA5) 652 transposase			0.14722	0.9036 0.34 0.9953 0.8176		0.3598	0.4011	0.5432 0.6664 0.7373	0.3085		0.8664 0.2053	0.7022 0.6153 0.1118 1.8983	1.063 0.7453	0.5796 0.0369	0.6234 U 0.0708 U	BAL3_95680035 BAL3_95680034 BAL3_95680034 BAL3_48660030	90 100 89
1RNA-Arg-TCG UBABSL4_7659G0005 UBABSL4_7659G0006 UBABSL4_7659G0006a UBABSL4_7659G0007	tRNA Arg TCG 447 Probable transposase 55 hypothetical protein 95 Conserved hypothetical protein 222 Conserved hypothetical protein				8.0075 12.4 1.3847 0.72 0.3207 0.2744 0.18	99			8.9624 1.4568 0.506 0.4331	0.4721 0.0152	66.616	4.2659 0.9011	11.817 5.5553 0.9267 1.0264	7.7624 0.9583	3.0499 0.4324	3.0805 0.1611 U	BAL3_80290025 BAL3_95320002 BAL3_95320001	100 99 99
UBABSL4_9211G0001 UBABSL4_9211G0002 UBABSL4_9211G0003 UBABSL4_9211G0005 UBABSL4_9211G0005 UBABSL4_9211G0007 UBABSL4_9211G0007 UBABSL4_9211G0008 UBABSL4_9211G0009	263 HNH endonuclease 131 HNH endonuclease 433 TPR-domain containing protein 118 3-dehydroquinate dehydratase, type II 192 translation elongation factor P 155 acetyl-CoA carboxylase, biotin carboxyl carrier 57 acetyl-CoA carboxylase, biotin carboxylase 205 acetyl-CoA carboxylase, biotin carboxylase 42 Thiamine-phosphate pyrophosphorylase ThiE	0.04689	0.25291	0.07773 0.11042 0.20923 0.04903 0.16948						0.0267 0.11 0.0376 0.1489 0.0141						U U U U U	BAL3_48660076 BAL3_95680090 BAL3_95680091 BAL3_95680091 BAL3_95680093 BAL3_95680093 BAL3_95680094 BAL3_95680094 BAL3_95680095	73 59 73 93 74 90 90
UBABSL4_10312G0001 UBABSL4_10312G0002 UBABSL4_10312G0003 UBABSL4_10312G0004 UBABSL4_10312G0005 UBABSL4_10312G0007 UBABSL4_10312G0007 UBABSL4_10312G0009 UBABSL4_10312G0009 UBABSL4_10376G0001 UBABSL4_10376G0002	238 Cation efflux system protein 656 excinuclease ABC, A subunit 186 excinuclease ABC, A subunit 240 outer membrane lipoprotein carrier protein LoIA 564 cell division FtsK 537 Metallo-beta-lactamase family protein 94 dimethyladenosine transferase 183 dimethyladenosine transferase 216 TonB family protein 171 hydrogenase accessory protein HypB 791 probable hydrogenase maturation protein HypF		0.00638 0.03349	0.04853						0.0088 0.0155 0.0077 0.0403 0.0158 0.0801 0.0253 0.0018				0.0058		U U U U U	BAL3_60500038 BAL3_60500037 BAL3_60500037 BAL3_60500036 BAL3_60500035 BAL3_60500033 BAL3_60500033 BAL3_60500033 BAL3_60500032	68 89 69 49 90 54 54
UBABSL4_10676G0003 UBABSL4_10676G0005 UBABSL4_10676G0006 UBABSL4_10676G0006 UBABSL4_10676G0007 UBABSL4_10676G0008	77 hydrogenase expression/formation protein HypC 53 hydrogenase expression/formation protein HypD 196 hydrogenase expression/formation protein HypD 352 Hydrogenase expression/formation protein HypE 287 High-affinity nickel-transporter 345 peptidase, M28 family									0.0074 0.0205 0.0151 0.0042								

UBABSL4_10676G0009	151 Ppx/GppA phosphatase							0.0764	4	UBAL3_94530005	69
UBABSL4_10718G0001	239 Conserved hypothetical protein							0.006			
UBABSL4_10718G0002	325 Putative transposase							0.0222	2	UBAL3_24060025	70
UBABSL4_10718G0003	134 Putative transposase									UBAL3_24060024	66
UBABSL4_10718G0004	188 Conserved hypothetical protein										
UBABSL4_10718G0005	39 hypothetical protein	ion								UBAL3 92050106	66
UBABSL4_10718G0006 UBABSL4_10718G0007	296 Probable sodium/calcium exchanger membrane reg415 Probable transporter protein	lion								UBAL3_92050106	59
UBABSL4_10718G0008	96 hypothetical protein									05/120_/2000100	07
UBABSL4_10718G0009	243 transposase										
UB 1 B 2 1 1 1 2 2 5 1 2 2 2 2 1											
UBABSL4_10954G0001 UBABSL4_10954G0002	305 Putative A/G-specific DNA glycosylase 264 Conserved hypothetical protein									UBAL3_82700015 UBAL3_82700014	57 63
UBABSL4_10954G0002 UBABSL4_10954G0003	153 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine	dinhosnho	kinase							UBAL3_82700013	59
UBABSL4_10954G0004	394 Aspartate aminotransferase (EC 2.6.1.1)	0.08588		0.54012				0.0256		UBAL3_82700012	86
UBABSL4_10954G0005	127 5-carboxymethyl-2-hydroxymuconate									UBAL3_82700011	63
UBABSL4_10954G0006	177 Dihydrodipicolinate reductase			0.05521				0.0571		UBAL3_82700010	84
UBABSL4_10954G0007	95 Dihydrodipicolinate reductase			0.09143				0.0607		UBAL3_82700010	55
UBABSL4_10954G0008	224 dihydrodipicolinate synthase		0.12022	0.02424				0.0322		UBAL3_82700009	78
UBABSL4_10954G0009	299 diaminopimelate decarboxylase		0.13233	0.19246				0.0531		UBAL3_82700007	86
UBABSL4_11165G0001	96 <mark>transcriptional regulator, LysR family</mark>		0.07494	0.05655				0.0301		UBAL3_95320053	88
UBABSL4_11165G0002	261 <mark>outer membrane efflux protein</mark>			0.03328				0.0111		UBAL3_95320055	87
UBABSL4_11165G0003	270 outer membrane efflux protein	0.05013						0.0053		UBAL3_95320055	
UBABSL4_11165G0004	253 Conserved protein of unknown function		0.01422	0.01717				0.0057		UBAL3_95320056	62
UBABSL4_11165G0005 UBABSL4_11165G0006	161 Conserved protein of unknown function 195 ABC transporter, ATPase subunit							0.0269	,	UBAL3_95320057 UBAL3_95320058	67 71
UBABSL4_11165G0007	274 ABC-2 type transporter									UBAL3_95320059	82
UBABSL4_11165G0008	245 oxidoreductase FAD/NAD(P)-binding domain			0.00886				0.0471		UBAL3_95320060	64
UBABSL4_11165G0009	210 Conserved protein of unknown function							0.0069		UBAL3_95320060a	a 45
UBABSL4_11484G0001	117 hypothetical protein							0.0863			
UBABSL4_11484G0001 UBABSL4_11484G0002	461 transposase							0.0663			
UBABSL4_11484G0003	81 hypothetical protein							0.0701			
UBABSL4_11484G0004	216 Conserved hypothetical protein							0.0267	7		
UBABSL4_11484G0005	142 phosphoribosyltransferase							0.0406		UBAL3_44810094	57
UBABSL4_11484G0006	153 heat shock protein Hsp20							0.0189)	UBAL3_74420024	56
UBABSL4_11484G0007 UBABSL4_11484G0008	241 Conserved hypothetical protein 64 hypothetical protein									UBAL3_92050050	52
UBABSL4_11484G0009	419 Conserved hypothetical protein										
_	,										
UBABSL4_11784G0001	177 Conserved protein of unknown function							0.0082		UBAL3_69480040	42
UBABSL4_11784G0002	518 glucose-6-phosphate 1-dehydrogenase	0.06888	0.01042					0.0306 0.0477		UBAL3_69480039	81 70
UBABSL4_11784G0003 UBABSL4_11784G0004	393 bifunctional transaldolase/phosoglucose isomerase 257 transketolase	0.06000	0.15102 0.04899					0.0477		UBAL3_69480038 UBAL3_69480037	70 78
UBABSL4_11784G0005	400 transketolase		0.04077	0.00543				0.1118		UBAL3_69480037	78
UBABSL4_11784G0006	136 squalene-hopene cyclase									UBAL3_69480035	79
UBABSL4_11784G0007	511 squalene-hopene cyclase							0.0367	7	UBAL3_69480035	79
UBABSL4_11784G0008	237 Conserved protein of unknown function			0.01205				0.0074		UBAL3_69480034	41
UBABSL4_11784G0009	392 Conserved protein of unknown function			0.01385				0.0074	1	UBAL3_69480033	86
UBABSL4_15692G0001	144 Conserved hypothetical protein	2.49087	0.49958	0.39962	7.1926 32.06	0.2601 0.4	4206 1.8753 5.0	077 3.3762	3.8311 0.7552 1.0246 2.9241	1.9509	
UBABSL4_15692G0002	64 Conserved hypothetical protein				1.9039 7.527	4 0.5853		255 2.9755			
UBABSL4_15692G0003	72 hypothetical protein							451 0.0601			
UBABSL4_15692G0004 UBABSL4_15692G0005	72 hypothetical protein 291 Conserved hypothetical protein				0.1047			451 0.1202 811 0.1041			50
UBABSL4_15692G0006	41 hypothetical protein				0.1047		0.8	0.0352		0.0601 UBAL3_92050097 0.0533	30
UBABSL4_15692G0007	587 putative type IV secretory pathway VirD4 componen	ts			0.0519		0.9	828 0.0098			
UBABSL4_15692G0008	282 hypothetical protein				0.108			502	0.3823 0.1469 0.4119 0.091		
UBABSL4_15692G0009	69 hypothetical protein				0.2207		1.3	935	0.1379 0.273 0.0744	0.0317	
LIB A BSL 4 190 4C0001	E4 hypothetical protein										
UBABSL4_1894G0001 UBABSL4_1894G0002	54 hypothetical protein 163 6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (F	liboflavin e	vnthase)	0.27976				0.0531		UBAL3_96150011	65
	,		,	,, 0				3,0001		2220_, 0.00011	30

UBABSL4_1894G0003 UBABSL4_1894G0004 UBABSL4_1894G0005 UBABSL4_1894G0006 UBABSL4_1894G0007 UBABSL4_1894G0008	51 GTP cyclohydrolase II 195 GTP cyclohydrolase II 272 NAD+ synthase 261 NAD+ synthase 173 Putative thioredoxin family protein 306 Alcohol dehydrogenase, zinc-binding domain		0.07053	0.12774 0.08352 0.03992			0.0212 0.0829 0.0167 0.0236	UBAL3_96150010 UBAL3_96150010 UBAL3_96150009 UBAL3_96150009 UBAL3_96150008 UBAL3_96150007	88 97 80 80 69
UBABSL4_2345G0001 UBABSL4_2345G0003 UBABSL4_2345G0004 UBABSL4_2345G0004a UBABSL4_2345G0005 fRNA-Asn-GIT	36 hypothetical protein 331 Conserved protein of unknown function 384 lysine 2,3-aminomutase YodO family protein 206 Conserved protein of unknown function 210 Putative 2-deoxycytidine 5-triphosphate deaminase tRNA Asn GTI	0.09668		0.00656 0.01054 0.1034			0.0488	UBAL3_57480017 UBAL3_57480016 UBAL3_57480017 UBAL3_57480014	69 81 88 91
UBABSL4_2345G0006 UBABSL4_2345G0007	165 Conserved protein of unknown function 117 Conserved protein of unknown function						0.0525 0.0123	UBAL3_48660006 UBAL3_48660006	37 42
UBABSL4_2429G0001 UBABSL4_2429G0002 UBABSL4_2429G0003 UBABSL4_2429G0004 UBABSL4_2429G0005 UBABSL4_2429G0006 UBABSL4_2429G0007 UBABSL4_2429G0008	204 hypothetical protein 181 hypothetical protein 962 malto-oligosyltrehalose synthase 556 Trehalose synthase (EC 5.4.99.16) 328 Trehalose synthase (EC 5.4.99.16) 157 Trehalose synthase (EC 5.4.99.16) 158 glycogen debranching enzyme GlgX 411 glycogen debranching enzyme GlgX		0.07439	0.01016 0.00391 0.07133	0.0911	4.73 0.1641 0.467	0.0424 0.0319 0.009 0.0467 9 0.0308 0.0372 5 0.2455	UBAL3_93200071 UBAL3_94530062	73 81 76 96
UBABSL4_7963G0001 UBABSL4_7963G0002 UBABSL4_7963G0003 UBABSL4_7963G0004 UBABSL4_7963G0005 UBABSL4_7963G0006	140 Conserved hypothetical protein 52 hypothetical protein 166 hypothetical protein 67 hypothetical protein 90 Conserved hypothetical protein 376 Conserved hypothetical protein		0.01570	0.01.400			0.0555 0.0861 0.0345	UBAL3_94240134	54 93
UBABSL4_7963G0007 UBABSL4_7963G0008	228 ABC transporter related 163 efflux transporter, RND family, MFP subunit		0.01578	0.01429			0.0253	UBAL3_94240137 UBAL3_94240138	85 75
UBABSL4_9214G0001 UBABSL4_9214G0002 UBABSL4_9214G0003 UBABSL4_9214G0004 UBABSL4_9214G0005 UBABSL4_9214G0006 UBABSL4_9214G0007 UBABSL4_9214G0008	233 Putative P-loop ATPase protein family 46 sigma 54 modulation protein/ribosomal protein 139 sigma 54 modulation protein/ribosomal protein 297 RNA polymerase, sigma 54 subunit, RpoN 249 ABC transporter, ATP-binding protein 220 Putative OstA family protein 123 Conserved protein of unknown function 296 malate dehydrogenase		1.29386 0.01211 0.0939 0.40101	0.16134			0.0186 0.1038 0.0534 0.0116 0.0459 0.0235 0.2242	UBAL3_44810086 UBAL3_44810087 UBAL3_44810087 UBAL3_44810089 UBAL3_44810099 UBAL3_44810090 UBAL3_44810091 UBAL3_44810092	72 93 86 76 90 80 72 98
UBABSL4_10878G0001 UBABSL4_10878G0002 UBABSL4_10878G0003 UBABSL4_10878G0004 UBABSL4_10878G0005 UBABSL4_10878G0006 UBABSL4_10878G0007 UBABSL4_10878G0007 UBABSL4_10878G0008	175 alanyl-tRNA synthetase 167 Holliday junction resolvase YagF 346 aminodeoxychorismate lyase 361 valyl-tRNA synthetase 441 valyl-tRNA synthetase 122 nicotinate-nucleotide pyrophosphorylase 60 nicotinate-nucleotide pyrophosphorylase 241 biotinacetyl-CoA-carboxylase ligase						0.0082 0.0173 0.0042 0.0196 0.0236	UBAL3_44810104 UBAL3_44810103 UBAL3_44810102 UBAL3_44810101 UBAL3_44810101 UBAL3_44810100 UBAL3_44810100 UBAL3_44810109	58 51 69 77 71 69 69 45
UBABSL4_10992G0001 UBABSL4_10992G0002 UBABSL4_10992G0003 UBABSL4_10992G0004 UBABSL4_10992G0005 UBABSL4_10992G0006 UBABSL4_10992G0007 UBABSL4_10992G0008	151 Formyltetrahydrofolate deformylase 137 1-acyl-sn-glycerol-3-phosphate acyltransferase 281 1-acyl-sn-glycerol-3-phosphate acyltransferase 134 Conserved hypothetical protein 142 Conserved hypothetical protein 108 histidinol-phosphate aminotransferase 178 histidinol-phosphate aminotransferase 65 sigma54 specific transcriptional regulator, Fis family						0.0191 0.0105 0.0051 0.0215 0.0305 0.0267 0.0081	UBAL3_94240089 UBAL3_94240080 UBAL3_94240082 UBAL3_94240091	70 78 62 52
UBABSL4_11318G0001 UBABSL4_11318G0003 UBABSL4_11318G0004	410 Conserved hypothetical protein 139 hypothetical protein 414 major facilitator superfamily transporter						0.0106 0.0104 0.0035	UBAL3_95450027	60

UBABSL4_11318G0005 UBABSL4_11318G0006 UBABSL4_11318G0007 UBABSL4_11318G0008 UBABSL4_11318G0009	241 glycosyl transferase, family 9 215 two component transcriptional regulator, LuxR 101 periplasmic sensor signal transduction histidine kinase 222 periplasmic sensor signal transduction histidine kinase 217 amino acid permease					0.012 0.0201		UBAL3_95450026 UBAL3_95450025 UBAL3_95450024 UBAL3_95450024 UBAL3_95450023	59 77 80 80 79
UBABSL4_11388G0001 UBABSL4_11388G0002 UBABSL4_11388G0003	450 TRNA-i(6)A37 modification enzyme (MiaB) 117 Conserved protein of unknown function 193 Putative SAM-dependent methyltransferases			0.01125		0.0289 0.0123 0.0299		UBAL3_95320041 UBAL3_95320040 UBAL3_95320039	75 51 67
UBABSL4_11388G0004 UBABSL4_11388G0005 UBABSL4_11388G0006 UBABSL4_11388G0007 UBABSL4_11388G0008	101 hypothetical protein 608 permease YjgP/YjgQ family protein 284 Ferrochelatase 182 Conserved protein of unknown function 164 Conserved protein of unknown function	1.26428 1.65064		0.60253		0.0143 0.8957 1.513		UBAL3_95320037 UBAL3_95320036 UBAL3_95320030 UBAL3_95320030	80 63 82 88
UBABSL4_11553G0001 UBABSL4_11553G0001 UBABSL4_11553G0002	63 Rod shape-determining protein MreC 172 Conserved hypothetical protein	1.03004	J.J7216	0.60706		0.0687 0.0084		UBAL3_94530044 UBAL3_94530043	63 42
UBABSL4_11553G0003 UBABSL4_11553G0004 UBABSL4_11553G0005	615 Peptidoglycan glycosyltransferase 364 Putative rod shape-determining protein (RodA) 522 Ribonucleases G and E	0.31116 (0.44789	0.57823		0.0193		UBAL3_94530042 UBAL3_94530041 UBAL3_94530040	71 56 87
UBABSL4_11553G0006 UBABSL4_11553G0007 UBABSL4_11553G0008	280 Conserved hypothetical protein 95 dihydroneopterin aldolase 301 Putative cobalamin B12-binding/Radical SAM family	protein	0.2151	0.03429 0.19118		0.0052 0.3643		UBAL3_94530037 UBAL3_94530038 UBAL3_94530035	76 55 93
UBABSL4_11778G0001 UBABSL4_11778G0002	46 hypothetical protein 192 Conserved protein of unknown function					0.0301		UBAL3_94240071	81
UBABSL4_11778G0003 UBABSL4_11778G0004 UBABSL4_11778G0005	302 transposase 318 hypothetical protein 72 transposase			0.01024	0.2123	0.1003 0.0408			
UBABSL4_11778G0006 UBABSL4_11778G0007 UBABSL4_11778G0008	268 peptidase U62, modulator of DNA gyrase 116 peptidase U62, modulator of DNA gyrase 237 peptidase U62, modulator of DNA gyrase	(0.01518	0.05956		0.0161		UBAL3_74420073 UBAL3_74420073 UBAL3_74420072	75 68 94
UBABSL4_11796G0001 UBABSL4_11796G0002 UBABSL4_11796G0003	168 GCN5-related N-acetyltransferase 93 hypothetical protein 60 hypothetical protein					0.0172			
UBABSL4_11796G0004 UBABSL4_11796G0005 UBABSL4_11796G0006	55 hypothetical protein 115 hypothetical protein 59 hypothetical protein						0.0276		
UBABSL4_11796G0007 UBABSL4_11796G0008	209 histidinol-phosphate phosphatase family protein 42 hypothetical protein							LID 4 LO 0 C / 000 CO	58
								UBAL3_95680059	
UBABSL4_11938G0001 UBABSL4_11938G0002 UBABSL4_11938G0003	166 Conserved protein of unknown function 204 Conserved protein of unknown function 425 Conserved hypothetical protein							UBAL3_44810050 UBAL3_44810049 UBAL3_44810048	69 67 71
UBABSL4_11938G0002 UBABSL4_11938G0003 UBABSL4_11938G0004 UBABSL4_11938G0005 UBABSL4_11938G0006	166 Conserved protein of unknown function 204 Conserved protein of unknown function 425 Conserved hypothetical protein 335 Putative twitching motility protein (PiIT) 142 Conserved hypothetical protein 58 hypothetical protein							UBAL3_44810050 UBAL3_44810049 UBAL3_44810048 UBAL3_44810047 UBAL3_44810046	69 67 71 81 72
UBABSL4_11938G0002 UBABSL4_11938G0003 UBABSL4_11938G0004 UBABSL4_11938G0005	146 Conserved protein of unknown function 204 Conserved protein of unknown function 425 Conserved hypothetical protein 335 Putative twitching motility protein (PiIT) 142 Conserved hypothetical protein					0.4134		UBAL3_44810050 UBAL3_44810049 UBAL3_44810048 UBAL3_44810047	69 67 71 81
UBABSL4_11938G0002 UBABSL4_11938G0003 UBABSL4_11938G0004 UBABSL4_11938G0005 UBABSL4_11938G0006 UBABSL4_11938G0007 UBABSL4_11938G0008 UBABSL4_12002G0001 UBABSL4_12002G0002	166 Conserved protein of unknown function 204 Conserved protein of unknown function 425 Conserved hypothetical protein 335 Putative twitching motility protein (PiIT) 142 Conserved hypothetical protein 58 hypothetical protein 136 Conserved hypothetical protein 171 transposase 243 Conserved hypothetical protein 214 Ribonuclease HII	0.75844	1 65893	2 40549		0.4134		UBAL3_44810050 UBAL3_44810049 UBAL3_44810048 UBAL3_44810047 UBAL3_44810046 UBAL3_44810045 UBAL3_78220010 UBAL3_78220009	69 67 71 81 72 79
UBABSL4_11938G0002 UBABSL4_11938G0003 UBABSL4_11938G0005 UBABSL4_11938G0006 UBABSL4_11938G0007 UBABSL4_11938G0008 UBABSL4_12002G0001 UBABSL4_12002G0001 UBABSL4_12002G0002 UBABSL4_12002G0003 UBABSL4_12002G0004 UBABSL4_12002G0005	166 Conserved protein of unknown function 204 Conserved protein of unknown function 425 Conserved hypothetical protein 335 Putative twitching motility protein (PiIT) 142 Conserved hypothetical protein 58 hypothetical protein 136 Conserved hypothetical protein 171 transposase 243 Conserved hypothetical protein 171 transposase 243 Conserved hypothetical protein 174 Ribonuclease HII 175 Ribosomal protein L19 243 tRNA (guanine-N1)-methyltransferase 187 Probable 16S rRNA processing protein RimM	0.75844	1.65893					UBAL3_44810050 UBAL3_44810049 UBAL3_44810047 UBAL3_44810046 UBAL3_44810045 UBAL3_78220010 UBAL3_78220009 UBAL3_78220008 UBAL3_78220007 UBAL3_78220006	69 67 71 81 72 79 40 59 89 71 61
UBABSL4_11938G0002 UBABSL4_11938G0003 UBABSL4_11938G0005 UBABSL4_11938G0006 UBABSL4_11938G0007 UBABSL4_11938G0008 UBABSL4_12002G0001 UBABSL4_12002G0001 UBABSL4_12002G0002 UBABSL4_12002G0003 UBABSL4_12002G0003	166 Conserved protein of unknown function 204 Conserved protein of unknown function 425 Conserved hypothetical protein 335 Putative twitching motility protein (PiII) 142 Conserved hypothetical protein 58 hypothetical protein 136 Conserved hypothetical protein 171 transposase 243 Conserved hypothetical protein 214 Ribonuclease HII 116 Ribosomal protein L19 243 tRNA (guanine-N1)-methyltransferase	C	0.01828	2.40549 0.03147 0.07503 1.10022		0.0178		UBAL3_44810050 UBAL3_44810049 UBAL3_44810048 UBAL3_44810046 UBAL3_44810046 UBAL3_44810045 UBAL3_78220010 UBAL3_78220009 UBAL3_78220008 UBAL3_78220008 UBAL3_78220007	69 67 71 81 72 79 40 59 89 71
UBABSL4_11938G0002 UBABSL4_11938G0003 UBABSL4_11938G0004 UBABSL4_11938G0006 UBABSL4_11938G0007 UBABSL4_11938G0008 UBABSL4_12002G0001 UBABSL4_12002G0001 UBABSL4_12002G0003 UBABSL4_12002G0003 UBABSL4_12002G0004 UBABSL4_12002G0006 UBABSL4_12002G0006 UBABSL4_12002G0006 UBABSL4_12002G0007	166 Conserved protein of unknown function 204 Conserved protein of unknown function 425 Conserved hypothetical protein 335 Putative twitching motility protein (PiIT) 142 Conserved hypothetical protein 58 hypothetical protein 136 Conserved hypothetical protein 171 transposase 243 Conserved hypothetical protein 214 Ribosomal protein L19 243 tRNA (guanine-N1)-methyltransferase 187 Probable 165 rRNA processing protein RimM 69 Ribosomal protein S16 492 signal recognition particle protein	C	0.01828	0.03147 0.07503		0.0178		UBAL3_44810050 UBAL3_44810049 UBAL3_44810047 UBAL3_44810045 UBAL3_44810045 UBAL3_78220010 UBAL3_78220009 UBAL3_78220007 UBAL3_78220007 UBAL3_78220005 UBAL3_78220005 UBAL3_78220005 UBAL3_78220004	69 67 71 81 72 79 40 59 89 71 61 78 77

UBABSL4_12137G0004 UBABSL4_12137G0005 UBABSL4_12137G0006 UBABSL4_12137G0007	68 Conserved hypothetical protein 405 Conserved protein of unknown function 131 Conserved protein of unknown function 648 ribonuclease R		0.0067	0.0849 0.0214 0.0551 0.064 <i>6</i>			UBAL3_94320045 UBAL3_94320046 UBAL3_94320047 UBAL3_94320048	83 64 81 83
UBABSL4_13030G0001	60 hypothetical protein							
UBABSL4_13030G0002 UBABSL4_13030G0003	152 hypothetical protein 63 Transposase						UBAL3_95390014	75
UBABSL4_13030G0004	331 Transposase						UBAL3_95390014	78
UBABSL4_13030G0005	520 Resolvase helix-turn-helix domain protein			0.0028			UBAL3_95530030	63
UBABSL4_13030G0006	64 Conserved hypothetical protein						LIPAL2 40470014	11
UBABSL4_13030G0007 UBABSL4_13030G0008	214 Conserved hypothetical protein 252 IstB domain protein ATP-binding protein			0.0057			UBAL3_49470014 UBAL3_95530028	66 86
UBABSL4_440G0001 UBABSL4_440G0002	258 Conserved hypothetical protein 121 Conserved hypothetical protein			0.0119	0.0246	54	UBAL3_95390007 UBAL3_95390005	90 98
UBABSL4_440G0002	369 Conserved hypothetical protein			0.0039			UBAL3_95390004	95
UBABSL4_440G0004	99 hypothetical protein							
UBABSL4_440G0005	85 Conserved hypothetical protein						UBAL3_95390003	60
UBABSL4_440G0006 UBABSL4_440G0007	519 transposase 261 hypothetical protein							
UBABSL4_774G0001	132 Homoserine dehydrogenase			0.0546			UBAL3_95450115	62
UBABSL4_774G0002 UBABSL4_774G0003	153 Conserved protein of unknown function 253 Aspartate aminotransferase (EC 2.6.1.17)			0.066 0.114			UBAL3_95450116 UBAL3_95450117	81 80
UBABSL4_774G0004	168 ProbableDeoR family transcriptional regulator							
UBABSL4_774G0005	105 Antibiotic biosynthesis monooxygenase						UBAL3_48660032	74
UBABSL4_774G0006 UBABSL4_774G0007	146 Conserved hypothetical protein 53 Conserved hypothetical protein			0.0692				
05/15024_// 40000/	do consorted hypotholical protein							
UBABSL4_1519G0001	44 hypothetical protein			0.0328			UBAL3_95680064	
UBABSL4_1519G0002 UBABSL4_1519G0002a	165 3-deoxy-D-manno-octulosonic-acid transferase 142 3-deoxy-D-manno-octulosonic-acid transferase			0.0175			UBAL3_95680065 UBAL3_95680065	54 72
UBABSL4_1519G0003	399 lipid-A-disaccharide synthase		0.00544	0.0036			UBAL3_95680067	63
UBABSL4_1519G0004	320 <mark>oxidoreductase domain protein</mark>	0.05058	0.01357	0.009			UBAL3_95680068	81
UBABSL4_1519G0005	114 Conserved protein of unknown function		0.05011	0.0074			UBAL3_95680069	80 85
UBABSL4_1519G0006	195 UDP-N-acetylglucosamine acyltransferase		0.05011	0.0074			UBAL3_95680070	03
UBABSL4_1807G0001	247 Conserved protein of unknown function	0.1096 0.21844		0.0584			UBAL3_94240030	93
UBABSL4_1807G0003 UBABSL4_1807G0004	211 Conserved protein of unknown function	0.05114 0.11846		0.0137 0.1296			UBAL3_94240030 UBAL3_94240031	86
UBABSL4_1807G0004	167 Conserved protein of unknown function 333 transcriptional activator domain	0.11046	0.0173	0.0043			UBAL3_94240031	65
UBABSL4_1807G0006	421 transcriptional activator domain			0.0034			UBAL3_94240033	
UBABSL4_1807G0007 UBABSL4_1807G0008	83 hypothetical protein							
UBAB3L4_1807 G0008	88 hypothetical protein							
UBABSL4_2023G0002	168 Conserved protein of unknown function			0.0172			UBAL3_79320021	93
UBABSL4_2023G0003 UBABSL4_2023G0004	41 hypothetical protein 46 hypothetical protein			0.0314				
UBABSL4 2023G0005	145 phosphoglycerate mutase 1 family		0.11232	0.0514			UBAL3_79320020	79
UBABSL4_2023G0006	62 transposase						_	
UBABSL4_2023G0007 UBABSL4_2023G0008	108 Conserved protein of unknown function		0.0062	0.0289			UBAL3_79320019	66
UBAB3L4_2023G0006	350 Glycerol-3-phosphate dehydrogenase (NAD(P)(+))		0.0062	0.0269			UBAL3_79320018	80
UBABSL4_2518G0001	119 Sel1 domain protein repeat-containing protein						UBAL3_95450104	68
UBABSL4_2518G0002 UBABSL4_2518G0002a	46 hypothetical protein			0.0314 0.0285				
UBABSL4_2518G0002d	152 probable cation diffusion facilitator family transporter242 TRNA/rRNA methyltransferase (SpoU)			0.0283			UBAL3_95450105	68
UBABSL4_2518G0004	456 cysteinyl-tRNA synthetase		0.00476	0.019			UBAL3_95450106	76
UBABSL4_2518G0005	217 Survival protein SurE			0.0133			UBAL3_95450107	78
tRNA-Pro-GGG	tRNA Pro GGG							
UBABSL4_3692G0001	273 Probable binding-protein-dependent transport system	ns inner membrane	component				UBAL3_82700020	69
UBABSL4_3692G0002	89 Probable binding-protein-dependent transport system	ns inner membrane	component				UBAL3_82700020	86

UBABSL4_3692G0003 UBABSL4_3692G0004 UBABSL4_3692G0005 UBABSL4_3692G0006 UBABSL4_3692G0007	255 ABC transporter, ATP-binding protein 161 Probable ABC transporter ATP-binding protein 81 Conserved protein of unknown function 286 Putative DNA processing protein DprA 455 DNA topoisomerase I	0.01976	0.04773	0.0057 0.0356 0.0202 0.0095	UBAL3_82700021 UBAL3_82700022 UBAL3_82700022a UBAL3_82700023 UBAL3_82700024	88 77 73 63 78
UBABSL4_6051G0001 UBABSL4_6051G0002	274 Probable ABC transporter permease protein 460 HNH endonuclease domain protein			0.0031	UBAL3_93670007	65
UBABSL4_6051G0003 UBABSL4_6051G0004 UBABSL4_6051G0005	40 hypothetical protein 265 Undecaprenyl-phosphate galactosephosphotransfer 142 Undecaprenyl-phosphate galactosephosphotransfer				UBAL3_24060027 UBAL3_24060027	62 64
UBABSL4_6051G0006 UBABSL4_6051G0007	406 Putative glycosyl transferase, group 1 508 Putative glycosyl transferase			0.0227	UBAL3_24060028	68
UBABSL4_9270G0001 UBABSL4_9270G0002	44 hypothetical protein 130 hypothetical protein					
UBABSL4_9270G0003 UBABSL4_9270G0004	224 hypothetical protein 259 type IV pilus assembly PilZ				UBAL3_95680084	49
UBABSL4_9270G0005	112 metal dependent phosphohydrolase			0.0129	UBAL3_95680083	84
UBABSL4_9270G0006 UBABSL4_9270G0008	193 D-lactate dehydrogenase (Cytochrome) 357 D-lactate dehydrogenase (Cytochrome)		0.00608	0.0224 0.0162	UBAL3_95680082 UBAL3_95680082	67 76
UBAB3L4_72/UGUU08	537 D-Idelate deflydrogeriase (Cylochionie)		0.00606	0.0162	UBAL3_73000002	70
UBABSL4_10021G0001 UBABSL4_10021G0002	173 hypothetical protein (TN)				100	
UBABSL4_10021G0002	59 hypothetical protein 404 glutamate-1-semialdehyde-2,1-aminomutase	0.0335 0.34723	0.38162	0.0321	UBAL3_79520070	85
UBABSL4_10021G0004	174 Cytidylyltransferase family protein			0.0083	UBAL3_79520068	71
UBABSL4_10021G0005 UBABSL4_10021G0006	241 transcription-repair coupling factor	0.01493	0.01802	0.0045	UBAL3_79520067	68 59
UBABSL4_10021G0006	321 transcription-repair coupling factor 214 transcription-repair coupling factor			0.0045	UBAL3_79520067 UBAL3_79520067	39
UB - BOL - 1001 5 00001				0.0004		4
UBABSL4_10815G0001 UBABSL4_10815G0002	89 Conserved hypothetical protein 263 Conserved protein of unknown function			0.0324 0.0165	UBAL3_94240108 UBAL3_94240107	61 83
UBABSL4_10815G0003	306 Conserved protein of unknown function			0.0100	UBAL3_94240107	66
UBABSL4_10815G0004	432 hypothetical protein					
UBABSL4_10815G0005 UBABSL4_10815G0006	370 glycosyl transferase, family 2 218 Putative methyltransferase				UBAL3_94240102 UBAL3_80630020	36 34
UBABSL4_10815G0007	277 glycosyl transferase, family 2			0.0052	UBAL3_94240103	57
UBABSL4_10926G0001	119 Conserved protein of unknown function				UBAL3_93200075	44
UBABSL4_10926G0001	98 peptidase M24				UBAL3_93200076	84
UBABSL4_10926G0003	296 peptidase M24	0.09145 0.01823		0.039	UBAL3_93200076	75
UBABSL4_10926G0004 UBABSL4_10926G0005	210 O-methyltransferase family protein 100 Putative rieske iron-sulfur family protein	0.16113 0.55667	1.01853 0.46687	0.1305 0.1587	UBAL3_93200077 UBAL3_93200080	78 75
UBABSL4_10926G0006	304 beta-lactamase domain protein		0.40007	0.1007	UBAL3_93200081	57
UBABSL4_10926G0007	40 hypothetical protein					
UBABSL4_11175G0001	71 Diaminopimelate epimerase		0.03058		UBAL3_80630101	79
UBABSL4_11175G0002	225 Conserved protein of unknown function				UBAL3_80630102	47
UBABSL4_11175G0003 UBABSL4_11175G0004	349 Alcohol dehydrogenase GroES domain protein				UBAL3_80630103 UBAL3_80630104	71 58
UBABSL4_11175G0004 UBABSL4_11175G0005	129 short-chain dehydrogenase/reductase SDR 117 transcriptional regulator, TraR/DksA family				UBAL3_80630104	80
tRNA-Ser-CGA	tRNA Ser CGA					
UBABSL4_11175G0006	112 Putative sigma-54 specific transcriptional regulator, Fi	is family		0.0129	UBAL3_80630105a	48
UBABSL4_11217G0001	245 phosphoribosylaminoimidazolecarboxamide formylh	ransferase	0.07977	0.0236	UBAL3_95680037	71
UBABSL4_11217G0002 UBABSL4_11217G0003	138 hypothetical protein 73 probable transcriptional regulator			0.0593		
UBABSL4_11217G0003	633 glycosyl transferase, family 39			0.0073	UBAL3_95680038	57
UBABSL4_11217G0005	408 Probable glycosyl transferase, family 9			0.0177	UBAL3_95680041	82
UBABSL4_11217G0006 UBABSL4_11217G0007	197 Conserved protein of unknown function 279 Conserved protein of unknown function			0.0439	UBAL3_95680042 UBAL3_95680042	70 70
OB/ (BSE4_1121/ G000/	277 GOLDGITGE PROTORT OF OTINIOWIT INTICITOT				0B/(L0_/3000042	, 0
UBABSL4_11218G0001	137 4-hydroxy-3-methylbut-2-en-1-yl diphosphate syntho	<u> </u>	0.11095	0.0105	UBAL3_92050032	93
UBABSL4_11218G0002	345 Peptidase M50, putative membrane-associated zinc	metallopeptidase		0.0084	UBAL3_92050031	79

UBABSL4_11218G0003 UBABSL4_11218G0004 UBABSL4_11218G0005 UBABSL4_11218G0006 UBABSL4_11218G0007	353 1-deoxy-D-xylulose 5-phosphate reductoisomerase 112 phosphatidate cytidylyltransferase 152 phosphatidate cytidylyltransferase 265 Undecaprenyl diphosphate synthase (EC 2.5.1.31) 112 Conserved protein of unknown function	0.17224	0.0163 0.0129 0.038 0.0544 0.0129	UBAL3_92050030 80 UBAL3_92050029 73 UBAL3_92050029 73 UBAL3_92050028 84 UBAL3_92050027 75
UBABSL4_11286G0002 UBABSL4_11286G0003 UBABSL4_11286G0004 UBABSL4_11286G0005 UBABSL4_11286G0006 UBABSL4_11286G0007 UBABSL4_11286G0008	76 hypothetical protein 217 hypothetical protein 237 hypothetical protein 263 type I site-specific deoxyribonuclease, HsdR 764 type I site-specific deoxyribonuclease, HsdR 259 Conserved hypothetical protein 299 DNA polymerase, beta domain protein region	0.2004 0.1581 0.3529 0.1528	0.1329 0.0417 0.0066 0.0877 0.2028 0.0426 0.1204 0.021 0.853 0.0329 0.0482 0.2307 0.0397 0.5545 0.0456 0.027 1.7943 0.0891 0.3216 0.111 0.0424	0.0225 0.0101 9 0.0132 0.0289 0.0046 0.0477 0.0083 UBAL3_95660004 86 1 0.037 0.0403 0.0801 UBAL3_95660004 86 0.0242 0.2313 0.2448 UBAL3_95660002 43 0.0735 0.2118 0.2669 UBAL3_95660006 93
UBABSL4_11340G0001 UBABSL4_11340G0002 UBABSL4_11340G0003 UBABSL4_11340G0004 UBABSL4_11340G0005 UBABSL4_11340G0006	321 Conserved protein of unknown function 92 Arginine decarboxylase 420 Arginine decarboxylase 58 Spermine synthase 121 S-adenosylmethionine decarboxylase related 61 hypothetical protein	0.55815	0.009 0.0172 0.0596	UBAL3_44810113 52 UBAL3_44810112 86 UBAL3_44810112 91 UBAL3_44810111 79 UBAL3_44810110 87
UBABSL4_11340G0007 UBABSL4_11800G0001	51 Conserved protein of unknown function 427 Enolase (EC 4.2.1.11)	0.14742 0.32801	0.0283 0.0405	UBAL3_44810108 88 UBAL3_74420034 86
UBABSL4_11800G0003 UBABSL4_11800G0004 UBABSL4_11800G0005 UBABSL4_11800G0006 UBABSL4_11800G0007	168 Probable Cytochrome c, NapC/NirT family 218 Conserved protein of unknown function 497 glutamyl-tRNA(GIn) amidotransferase, B subunit 118 glutamyl-tRNA(GIn) amidotransferase, A subunit 254 glutamyl-tRNA(GIn) amidotransferase, A subunit	0.02533 0.07428	0.0945 0.0132 0.0232 0.0057	UBAL3_74420035 68 UBAL3_74420036 68 0.0034 UBAL3_74420037 76 UBAL3_74420038 74 UBAL3_74420038 74
UBABSL4_11800G0008 UBABSL4_11944G0001 UBABSL4_11944G0002	 50 hypothetical protein 67 Ribosomal protein L35 160 Translation initiation factor 3 (IF-3) 	1.91918	0.2584 0.1352	UBAL3_93200105a 94 UBAL3_93200106a 71
UBABSL4_11944G0003 UBABSL4_11944G0004 UBABSL4_11944G0005 UBABSL4_11944G0006 UBABSL4_11944G0007	79 threonyl-tRNA synthetase 595 threonyl-tRNA synthetase 287 Conserved protein of unknown function 305 Conserved protein of unknown function 658 amino acid permease	0.12091 0.09671	0.1278 0.0558 0.0452 0.0142 0.068	UBAL3_93200107 67 UBAL3_93200107 88 UBAL3_93200109 83 UBAL3_93200110 51 UBAL3_93200111 85
UBABSL4_12059G0001 UBABSL4_12059G0002 UBABSL4_12059G0003 UBABSL4_12059G0003	121 RNA-directed DNA polymerase (reverse transcriptase 228 Conserved hypothetical protein 282 metallo-beta-lactamase family protein 115 hypothetical protein	0.2004 0.1643 0.162	0.0703 0.0127 0.5702 0.79 0.4385 0.624 0.2787 0.3308 0.945	7 1.0646 0.4168 0.6464
UBABSL4_12059G0005 UBABSL4_12059G0006 UBABSL4_12059G0007	152 Conserved hypothetical protein 287 Conserved protein of unknown function 431 Putative helicase	0.1002 0.4246 0.1767		8 1.2185 0.3266 0.827 UBAL3_95450030 89 3 1.3126 0.656 1.1731 UBAL3_95450029 98 5 1.0998 0.5441 0.9333 UBAL3_95450028 98
UBABSL4_12190G0001 UBABSL4_12190G0002 UBABSL4_12190G0003 UBABSL4_12190G0004	142 Conserved protein of unknown function 186 Acireductone dioxygenase, ARD 206 Putative Ribulose-bisphosphate carboxylase-like 197 Putative Ribulose-bisphosphate carboxylase-like		0.0203 0.0465 0.028	UBAL3_92050113 89 UBAL3_92050112 60 UBAL3_92050111 61 UBAL3_92050111 74
UBABSL4_12190G0005 UBABSL4_12190G0006 UBABSL4_12190G0007	216 Probable hydrolase, haloacid dehalogenase-like fam 210 Putative aldolase class II 900 diguanylate cyclase/phosphodiesterase with PAS/PAG		0.0067	UBAL3_92050110 65 UBAL3_92050109 54
UBABSL4_12260G0001 UBABSL4_12260G0002	317 Putative proteasome component 67 Conserved protein of unknown function	0.00685	0.0501	UBAL3_92050099 62 UBAL3_92050100 68
UBABSL4_12260G0003 UBABSL4_12260G0004 UBABSL4_12260G0005 UBABSL4_12260G0006 UBABSL4_12260G0007	268 Putative 20S proteasome beta-subunit 231 Probable 20S proteasome alpha-subunit 446 Putative proteasome component 228 Conserved hypothetical protein 342 ATPase (AAA+ superfamily)-like	0.0094	0.0269 0.0562 0.055 0.0063	UBAL3_92050101 76 UBAL3_92050102 73 UBAL3_92050103 73 UBAL3_92050104 61 UBAL3_95680032 43
UBABSL4_12512G0001 UBABSL4_12512G0002	448 glycosyl transferase 650 lipopolysaccharide biosynthesis protein		0.0515 0.0355	UBAL3_94240120 59 UBAL3_94240121 84

UBABSL4_12512G0004 UBABSL4_12512G0005 UBABSL4_12512G0006	617 ABC transporter related 351 glycosyl transferase, family 2 421 Conserved hypothetical protein		0.0154	7					0.0047 0.0164 0.0206					UBAL3_94240122 UBAL3_94240123 UBAL3_94240124	81 80 79
UBABSL4_12512G0007 UBABSL4_12512G0008	60 hypothetical protein 257 UTP-glucose-1-phosphate uridylyltransferase	0	.014 0.0126	7					0.024 0.0112					UBAL3_94240125	98
UBAB\$L4_12616G0001	188 hypothetical protein		0.01733	3					0.0307						
UBABSL4_12616G0002	384 transposase			0.0397	0.7804			1.3771	0.2254				0.0089	0.0512	
UBABSL4_12616G0003	236 transposase														
UBABSL4_12616G0004	504 transposase										0.0103				
UBABSL4_12616G0006	181 hydrogenase maturation protease								0.00.47						
UBABSL4_12616G0007	433 [NiFe] hydrogenase large subunit HoxH								0.0067						
UBABSL4_12616G0008	35 hypothetical protein														
UBABSL4 12862G0001	302 3-hydroxyisobutyrate dehydrogenase	0.04482 0.28	3585 0.1438	0.5044			0.2235	0.6367	0.086	0.5354	0.3944	0.2495	0.2154	0.0507 UBAL3_95680118	88
UBABSL4_12862G0002	226 ABC transporter, ATP-binding protein			0.7414		0.268		0.1418						0.1354 UBAL3_95680119	98
UBABSL4_12862G0003	866 Putative permease			0.1407 0.0927	0.173			0.2776		0.465				0.0164 UBAL3_95680120	95
UBABSL4_12862G0004	370 Conserved protein of unknown function			0.2058				0.6063	0.0117	0.1628	0.14	0.0255	0.0509	0.0089 UBAL3_95680121	83
UBABSL4_12862G0005	341 glycosyl transferase, family 2				0.2197				0.0719		0.2278			0.0256 UBAL3_95680125	34
UBABSL4_12862G0006	286 Conserved protein of unknown function	0.04733 0.01	1258	0.8521	0.262			0.3922			0.3259		0.1795	0.0459 UBAL3_95680123	89
UBABSL4_12862G0007	436 Probable heptosyltransferase family protein			0.1397		0.2779		0.441	0.0629	0.1818	0.1663	0.0072	0.161	0.0627 UBAL3_95680124	92
UBABSL4_12929G0001	56 helix-turn-helix domain protein			0.272 16.489)			1 1444	0.1546	0.2831		0.3924	0.0917	0.0976 UBAL3 82700044	91
UBABSL4_12929G0002	1023 type I site-specific deoxyribonuclease, HsdR			0.2829 6.7891				1.3002			0.0405			0.031 UBAL3_82700045	90
UBABSL4_12929G0003	413 hypothetical protein			0.3319			0.3269	0.2328		0.1689		0.2736			, 0
UBABSL4_12929G0004	61 hypothetical protein							0.2627							
UBABSL4_12929G0005	404 Conserved hypothetical protein			0.1508 0.0994	1		0.3342	0.476	0.0214	0.0392	0.0128	0.0932	0.0593	0.0081	
UBABSL4_12929G0006	98 Conserved hypothetical protein			0.4663			0.6889		0.0147	0.4206		0.1922		0.0446 UBAL3_95530032	63
UBABSL4_12929G0007	399 Conserved hypothetical protein			0.1527			0.1692	1.4057	0.0615	0.4053	0.0389	0.4012	0.0815	0.0411 UBAL3_95530031	60
UBABSL4_1022G0001	62 Conserved hypothetical protein								0.0233					UBAL3 94320031	80
UBABSL4_1022G0001	413 NADH dehydrogenase (EC 1.6.99.3)								0.0233					UBAL3_94320030	00
UBABSL4_1022G0003	26 NADH dehydrogenase (EC 1.6.99.3)								0.0170					UBAL3_94320030	
UBABSL4_1022G0004	243 Conserved hypothetical protein													UBAL3_94320029	67
UBABSL4_1022G0005	218 Conserved hypothetical protein													UBAL3_94320029	
UBABSL4_1022G0006	66 hypothetical protein														
LID + DOL + 00 +0 00001															
UBABSL4_2042G0001 UBABSL4_2042G0002	81 hypothetical protein 270 Carbohydrate kinase family protein								0.0053					UBAL3_92050209	57
UBABSL4_2042G0002a	144 Carbohydrate kinase family protein								0.0033					UBAL3_92050209	57
UBABSL4_2042G0003	126 holo-acyl-carrier-protein synthase								0.0229					UBAL3_92050208	60
UBABSL4_2042G0004	244 Putative pyridoxal phosphate biosynthesis protein	0.05547												UBAL3_92050207	59
UBABSL4_2042G0005	117 Processing peptidase								0.037					UBAL3_92050206	77
		0.05004							0.10.10						0.7
UBABSL4_2194G0001 UBABSL4_2194G0003	DNA-directed RNA polymerase, beta subunit DNA-directed RNA polymerase, beta subunit	0.35296 0.96 0.22748 0.36	6652 0.4825						0.1243 0.0202					UBAL3_80150002 UBAL3_80150002	87 73
UBABSL4 2194G0004	130 Ribosomal protein L7/L12		3655 3.02339						0.0202					UBAL3_80150003	93
UBABSL4_2194G0005	174 Ribosomal protein L10		2067 0.23088						0.0415					UBAL3_80150004	82
UBABSL4_2194G0006	233 Ribosomal protein L1	0.34855 1.16							0.0124					UBAL3_80150005	83
UBABSL4_2194G0007	129 Ribosomal protein L11	0.62955 0.51	1584 0.81642	2										UBAL3_80150006	90
		0.10000		,										118.11.0.00.1000.10	
UBABSL4_3115G0001	223 Putative ATP-dependent Clp protease, ATPase subuni	0.18209 0.41	1937 0.2872	5					0.3752					UBAL3_80420043	91
UBABSL4_3115G0002 UBABSL4_3115G0003	130 hypothetical protein 55 Putative ATP-dependent Clp protease, ATPase subuni	+	0.03948	3					0.0999 0.1574					UBAL3_80420043	93
UBABSL4_3115G0004	346 biotin synthase		0.03946						0.1374					UBAL3_80420043	73 74
UBABSL4_3115G0005	104 6-carboxyhexanoateCoA ligase		3.00-10.	-					3.0200					UBAL3_80420041	60
UBABSL4_3115G0006	207 8-amino-7-oxononanoate synthase													UBAL3_80420040	57
UBABSL4_4360G0001	264 flagellar hook-length control protein								0.0219					UBAL3_80630062	55
UBABSL4_4360G0002 UBABSL4_4360G0004	233 flagellar hook capping protein FlgD 459 Probable flagellar hook protein FlgE	0.22116 0.00	0.007						0.0247					UBAL3_80630061 UBAL3_80630060	81 89
UBABSL4_4360G0004a	111 flagellar basal body-associated protein FliL	U.ZZ110 U.UL	77 U4 U.UU/						0.1331					UBAL3_80630059	78
UBABSL4_4360G0005	126 flagellar motor switch protein FliN	0.19	9983 0.2068						0.0801					UBAL3_80630058	90
UBABSL4_4360G0006	114 Conserved protein of unknown function								0.0633					UBAL3_80630057	83

UBABSL4_4700G0001 UBABSL4_4700G0002 UBABSL4_4700G0003 UBABSL4_4700G0004 UBABSL4_4700G0005 UBABSL4_4700G0006 UBABSL4_8602G0001 UBABSL4_8602G0001 UBABSL4_8602G0002 UBABSL4_8602G0003 UBABSL4_8602G0003	288 Conserved protein of unknown function 254 Conserved protein of unknown function 87 Conserved protein of unknown function 436 ATP-dependent Clp protease, ATP-binding subunit 202 ATP-dependent Clp protease, proteolytic subunit 363 trigger factor, N-terminal domain 161 Conserved protein of unknown function 225 Conserved hypothetical protein 81 Conserved hypothetical protein 178 Cobyrinic acid a,c-diamide synthase 215 metallophosphoesterase	0.12418		0.01 0.0332 0.0926 0.0357 0.0874 0.009 0.0128 0.	0.0279	UBAL3_92050166 UBAL3_92050164 UBAL3_92050163 UBAL3_92050161 UBAL3_92050161 UBAL3_92050160 0.0425 UBAL3_92050009a 0.0425 UBAL3_95660001a UBAL3_95390015 0.0096 0.0061 UBAL3_95390016 UBAL3_95390018	69 51 70 88 94 56 56 59 86 87 74
UBABSL4_9595G0001 UBABSL4_9595G0002 UBABSL4_9595G0003 UBABSL4_9595G0004 UBABSL4_9595G0005 UBABSL4_9595G0006	192 metallophosphoesterase 307 Putative filamentous haemagglutinin family protein 58 Conserved protein of unknown function 114 transposase 353 Conserved protein of unknown function 174 Conserved hypothetical protein 491 Conserved hypothetical protein			0.6391 0.4975 0.1012 0.6784 0.4228 0.0911	0.2685 0.0511 0.328 0.1112 0.0275 0.1168 0.0147 0.0356 0.2551	0.0089 0.0114 UBAL3_75390020 0.591 0.1923 UBAL3_78920045 0.2361 0.0754 UBAL3_78920044 0.045 0.3249 0.1115 UBAL3_78920048 0.3148 0.088 UBAL3_70870001 0.0314 0.0022 UBAL3_70870002	80 79 84 82 60 71
UBABSL4_9900G0001 UBABSL4_9900G0002 UBABSL4_9900G0003 UBABSL4_9900G0004 UBABSL4_9900G0005 UBABSL4_9900G0006	500 Conserved protein of unknown function 161 Conserved protein of unknown function 146 Conserved protein of unknown function 701 Conserved protein of unknown function 343 Conserved hypothetical protein 395 glycosyl transferase, group 1			0.0115		UBAL3_44810076 UBAL3_44810076 UBAL3_44810075 UBAL3_44810073 UBAL3_44810072 UBAL3_44810071	57 65 75 47 51 66
UBABSL4_10015G0001 UBABSL4_10015G0002 UBABSL4_10015G0003 UBABSL4_10015G0004 UBABSL4_10015G0006 UBABSL4_10015G0007	74 Radical SAM domain protein 347 ubiquinone/menaquinone biosynthesis methyltransfe 126 hypothetical protein 350 diguanylate cyclase 1613 diguanylate cyclase/phosphodiesterase with 154 phenylalanyl-tRNA synthetase, beta subunit	0.11419 0.06032 0.0564	0.107	0.0624 0.5725 0.0124 0.0018 0.0281		UBAL3_94530003 UBAL3_94530004 UBAL3_93200104 UBAL3_93200103 UBAL3_93200102	64 85 71 42 67
UBABSL4_10425G0001 UBABSL4_10425G0002 UBABSL4_10425G0003 UBABSL4_10425G0004 UBABSL4_10425G0005 UBABSL4_10425G0006	155 hypothetical protein 62 Conserved hypothetical protein 321 GTP-binding protein (EngA) 152 GTP-binding protein (EngA) 116 ATPase 49 ATPase			0.018 0.038		UBAL3_94320031 UBAL3_94320032 UBAL3_94320032 UBAL3_95450079 UBAL3_95450079	79 82 78 36 61
UBABSL4_10505G0001 UBABSL4_10505G0002 UBABSL4_10505G0003 UBABSL4_10505G0004 UBABSL4_10505G0005 UBABSL4_10505G0006	28 hypothetical protein 191 Conserved protein of unknown function 164 Phosphopantetheine adenylyltransferase 115 Aspartate aminotransferase 235 Aspartate aminotransferase 53 putative regulatory protein, FmdB family	0.05357 0.00924 0.3054		0.0616 0.0125		UBAL3_95680002 UBAL3_95680003 UBAL3_95680004 UBAL3_95680004 UBAL3_95680005	62 84 81 81
UBABSL4_10993G0001 UBABSL4_10993G0002 UBABSL4_10993G0003 UBABSL4_10993G0004 UBABSL4_10993G0005 UBABSL4_10993G0006	79 NUDIX hydrolase 103 Probable ferredoxin 477 sigma54 specific transcriptional regulator, Fis family 179 Anthranilate synthase component I 342 Anthranilate synthase component I 131 Anthranilate synthase component I	0.08414 0.05397		0.006 0.0161 0.038 0.011		UBAL3_94170006 UBAL3_94170007 UBAL3_94170008 UBAL3_94170009 UBAL3_94170009 UBAL3_94170010	59 55 76 57
UBABSL4_11152G0001 UBABSL4_11152G0002 UBABSL4_11152G0003 UBABSL4_11152G0004 UBABSL4_11152G0005 UBABSL4_11152G0007	136 Conserved protein of unknown function 415 major facilitator superfamily transporter 386 Probable threalose biosynthesis protein 271 alpha amylase, catalytic region 211 alpha amylase, catalytic region 194 glutamate decarboxylase	0.01854 0.02239		0.0106 0.0278 0.0053 0.0595		UBAL3_94530062a UBAL3_94530063 UBAL3_94530064 UBAL3_94530065 UBAL3_94530065 UBAL3_94530067	59 84 68 72 72

UBABSL4_11187G0001 UBABSL4_11187G0002 UBABSL4_11187G0003 UBABSL4_11187G0004 UBABSL4_11187G0005 UBABSL4_11187G0006	62 type II secretion system protein E 218 Conserved protein of unknown function 128 conserved hypothetical protein 343 Conserved hypothetical protein 272 hypothetical protein 315 Putative type II secretion system protein F												UI	BAL3_44810057 BAL3_44810058 BAL3_44810060	94 70 84
UBABSL4_11204G0001 UBABSL4_11204G0002 UBABSL4_11204G0003 UBABSL4_11204G0004	244 geranylgeranyl reductase 354 Probable protease family protein 391 primosomal protein N' 56 hypothetical protein												Ul	BAL3_94530015 BAL3_94530014 BAL3_94530013	63 53 62
UBABSL4_11204G0005 UBABSL4_11204G0006	157 Regulatory protein 171 Glycine hydroxymethyltransferase	0.1788	0.01383 0.30477				0.0	253						BAL3_94530012 BAL3_94530011	81 78
UBABSL4_11396G0001 UBABSL4_11396G0002 UBABSL4_11396G0003 UBABSL4_11396G0004 UBABSL4_11396G0005 UBABSL4_11396G0006	235 S-adenosyl-methyltransferase MraW 96 Conserved hypothetical protein 567 Peptidoglycan glycosyltransferase 330 UDP-N-acetylmuramoylalanyl-D-glutamate2, 6-diam 52 UDP-N-acetylmuramoyl-tripeptideD-alanyl-D-alanine	inopimelate ligase (0.1	.043 .503 .0087					UI UI UI	BAL3_92050132 BAL3_92050133 BAL3_92050134 BAL3_92050136 BAL3_92050136 BAL3_92050137	74 64 72 71 71 60
UBABSL4_11410G0001 UBABSL4_11410G0002 UBABSL4_11410G0002G UBABSL4_11410G0003 UBABSL4_11410G0004 UBABSL4_11410G0005	942 type III restriction enzyme, res subunit 271 Conserved hypothetical protein 186 CRISPR-associated protein, NE0113 family 156 Ankyrin 212 Conserved hypothetical protein 159 Conserved hypothetical protein	0.43382 0.18446	0.0696	0.097 0.2963 0.2457 0.1953 0.0718	0.	0.363 0. 4328 0. 0.	0851 0.0 1183 0.0 2585 0.1 2054 0.0 2268 0.0 1008 0.0	396 1925 1136	0.234 0.4262 0.5691 0.3739	0.3058 0.5568 0.8631 0.2687	0.7426 0.6439 0.8292	0.2526 0.1472 0.3511 0.1373	0.3872 UI 0.1234 UI 0.2803 UI 0.098 UI	BAL3_95450048 BAL3_95450049 BAL3_95450050 BAL3_95450052 BAL3_95450053 BAL3_95450054	76 96 98 96 88 98
UBABSL4_11422G0001 UBABSL4_11422G0002 UBABSL4_11422G0003 UBABSL4_11422G0004 UBABSL4_11422G0005 UBABSL4_11422G0006	590 Glycyl-1RNA synthetase, beta subunit 290 Glycyl-1RNA synthetase alpha subunit 62 Conserved protein of unknown function 111 transcriptional regulator, XRE family 31 hypothetical protein 218 ATPase, P-type (transporting), HAD superfamily,		0.00552 0.0337				0.0 0.3	.044 9448 956 013					UI UI	BAL3_95450156 BAL3_95450157 BAL3_80420077 BAL3_80420074 BAL3_74420008	64 76 82 79
UBABSL4_11513G0001 UBABSL4_11513G0002 UBABSL4_11513G0003 UBABSL4_11513G0004 UBABSL4_11513G0005 UBABSL4_11513G0006	286 Conserved hypothetical protein 595 DNA topoisomerase III 124 DNA topoisomerase III 319 hypothetical protein 238 icmL/dotl 43 hypothetical protein				6.3538 5.9046 2.4425 2.8483 4.0721 1.4087	0.	0.0	0101					Ul	BAL3_96120025 BAL3_96120026 BAL3_96120026	60 70 82
UBABSL4_11589G0001 UBABSL4_11589G0002 UBABSL4_11589G0003 UBABSL4_11589G0004 UBABSL4_11589G0006 UBABSL4_11589G0007	496 ATPase AAA-2 domain protein 293 Conserved hypothetical protein 492 Conserved hypothetical protein 138 Conserved hypothetical protein 139 GPW/gp25 family protein 149 Conserved protein of unknown function	0.04351 0.4542 1.08632	1.20963				0.0 0.0 0.0 0.0	0262 0049 0117 0209 0311					UI UI UI	BAL3_94240025 BAL3_94240026 BAL3_94240027 BAL3_94240027 BAL3_94240028 BAL3_94240029	90 81 78 78 88 95
UBABSL4_11671G0001 UBABSL4_11671G0002 UBABSL4_11671G0003 UBABSL4_11671G0004 UBABSL4_11671G0005 UBABSL4_11671G0006	397 Pyruvate:ferredoxin oxidoreductase alpha subunit (EC 48 hypothetical protein 204 Conserved protein of unknown function 165 Putative hydrogenase-3 subunit (HycG) 448 Putative hydrogenase-3 subunit (HycE) 456 Putative hydrogenase-4 subunit (HyfF)	0.15342 0.67499	0.12033 0.03726				0.1	526 556 0064					UI UI UI	BAL3_79520040 BAL3_79520041 BAL3_79520042 BAL3_79520043 BAL3_79520044	96 47 59 63 75
TRNA-Pro-CGG UBABSL4_11675G0001 UBABSL4_11675G0002 UBABSL4_11675G0003 UBABSL4_11675G0004 UBABSL4_11675G0005	tRNA Pro CGG 104 acylphosphatase 315 RNA polymerase, sigma 70 subunit, RpoD family 173 adenine phosphoribosyltransferase 104 Conserved protein of unknown function 389 major facilitator superfamily protein	0.03426 0.09356					0.0	0458 0334 0277 0074					UI UI UI	BAL3_95450135 BAL3_95450134 BAL3_95450133 BAL3_95450132 BAL3_95450131	44 69 70 59 62
UBABSL4_11713G0001	99 aspartyl-tRNA synthetase						0.0	146					UI	BAL3_94170058	72

UBABSL4_11713G0002 UBABSL4_11713G0003 UBABSL4_11713G0004 UBABSL4_11713G0005 UBABSL4_11713G0006 UBABSL4_11756G0001 UBABSL4_11756G0002	69 Conserved protein of unknown function 74 Conserved protein of unknown function 643 Pseudouridine synthase, Rsu 514 GMP synthase [glutamine-hydrolyzing] 159 inosine-5'-monophosphate dehydrogenase 60 hypothetical protein 345 phage integrase		0.01013 0.00845 0.01366	0.0056 0.0181	UBAL3_94170059 UBAL3_80150041 UBAL3_94170060 UBAL3_94170061 UBAL3_94170062	60 67 53 81 92
TRNA-Leu-CAG UBABSL4_11756G0003 UBABSL4_11756G0004 UBABSL4_11756G0005	tRNA Leu CAG 460 Fumarate hydratase, class II (EC 4.2.1.2) 109 Probable ferredoxin 472 cation transport ATPas	0.04301 (1.73848 0.77549 3		0.1066 0.4235 0.0092	UBAL3_78920008 UBAL3_78920007	88 94
UBABSL4_11866G0001 UBABSL4_11866G0002 UBABSL4_11866G0003 UBABSL4_11866G0004 UBABSL4_11866G0005 UBABSL4_11866G0006	32 hypothetical protein 236 uridylate kinase 185 ribosome recycling factor 408 alanine racemase 258 Putative integral membrane protein 262 ABC transporter AIP-binding protein	0.50296 (0.07316 0.22359 (0.1039 0.0234 0.0035 0.0056 0.011	UBAL3_94530026 UBAL3_94530025 UBAL3_94530024 UBAL3_94530023 UBAL3_94530022	92 83 53 82 75
UBABSL4_12078G0001 UBABSL4_12078G0002 UBABSL4_12078G0003 UBABSL4_12078G0004 UBABSL4_12078G0005 UBABSL4_12078G0006	133 Histidyl-tRNA lygase (EC 6.1.1.21) 545 D-3-phosphoglycerate dehydrogenase 220 aminotransferase, class V 126 aminotransferase, class V 285 Ankyrin 266 Phosphate butyryttransferase	0.02704 0.22352 0.55109 0 0.18802 0 0.26856 0.22838 0	0.54287	0.0217 0.0847 0.1836 0.1145 0.0051 0.0108	UBAL3_95320027 UBAL3_95320026 UBAL3_95320025 UBAL3_95320025 UBAL3_44810062 UBAL3_80420068	83 85 88 86 43 65
UBABSL4_12508G0001 UBABSL4_12508G0002 UBABSL4_12508G0003 UBABSL4_12508G0004 UBABSL4_12508G0005 UBABSL4_12508G0006	219 two component, sigma54 specific, transcriptional reg 474 Probable TPR-domain containing protein 625 Probable TPR-domain containing protein 264 Conserved protein of unknown function 291 UBA/THIF-type NAD/FAD binding protein 184 transposase	0.01362 (0.05562 (0.0132	UBAL3_94240128 UBAL3_94240129 UBAL3_94240129 UBAL3_94240130 UBAL3_94240131	79 73 63 67 73
	104 114113003436					
UBABSL4_13826G0001 UBABSL4_13826G0002 UBABSL4_13826G0004 UBABSL4_13826G0005 UBABSL4_13826G0006 UBABSL4_13826G0007	85 Conserved hypothetical protein 198 Conserved hypothetical protein 176 hypothetical protein 97 Conserved hypothetical protein 55 hypothetical protein 163 Conserved hypothetical protein				UBAL3_96270022 UBAL3_80290018	69 81
UBABSL4_13826G0001 UBABSL4_13826G0002 UBABSL4_13826G0004 UBABSL4_13826G0005 UBABSL4_13826G0006	85 Conserved hypothetical protein 198 Conserved hypothetical protein 176 hypothetical protein 97 Conserved hypothetical protein 55 hypothetical protein				_	
UBABSL4_13826G0001 UBABSL4_13826G0002 UBABSL4_13826G0004 UBABSL4_13826G0005 UBABSL4_13826G0006 UBABSL4_13826G0007 UBABSL4_435G0001 UBABSL4_435G0002 UBABSL4_435G0002 UBABSL4_435G0002 UBABSL4_435G0003	85 Conserved hypothetical protein 198 Conserved hypothetical protein 176 hypothetical protein 97 Conserved hypothetical protein 55 hypothetical protein 163 Conserved hypothetical protein 222 Probable antirepressor protein (Ant) 98 Putative cobyrinic acid a,c-diamide synthase 161 probable filamentation induced by cAMP protein Fic 321 ParB-like partition protein			0.0224	UBAL3_80290018 UBAL3_44810010 UBAL3_44810013 UBAL3_44810015	79 85 78
UBABSL4_13826G0001 UBABSL4_13826G0002 UBABSL4_13826G0004 UBABSL4_13826G0005 UBABSL4_13826G0007 UBABSL4_435G0001 UBABSL4_435G0002 UBABSL4_435G0002 UBABSL4_435G0003 UBABSL4_435G0004 UBABSL4_731G0001 UBABSL4_731G0002 UBABSL4_731G0002 UBABSL4_731G0002 UBABSL4_731G0003	85 Conserved hypothetical protein 198 Conserved hypothetical protein 176 hypothetical protein 97 Conserved hypothetical protein 55 hypothetical protein 163 Conserved hypothetical protein 163 Conserved hypothetical protein 222 Probable antirepressor protein (Ant) 98 Putative cobyrinic acid a,c-diamide synthase 161 probable filamentation induced by cAMP protein Fic 321 Par8-like partition protein 383 Probable DNA helicase 193 Conserved protein of unknown function 125 Probable general secretion pathway protein I 81 Probable general secretion pathway protein J 60 hypothetical protein				UBAL3_80290018 UBAL3_44810010 UBAL3_44810013 UBAL3_44810017 UBAL3_24060066 UBAL3_24060065	79 85 78 85 57 71

UBABSL4_1305G0001	75 phage integrase family protein			0.0423 0.045	6 0.0291 UBAL3_69480048	59
UBABSL4_1305G0002	238 Conserved hypothetical protein		0.0364	0.04 0.0132 0.122	3 0.0827	
UBABSL4_1305G0003	125 Conserved protein of unknown function				0.0087 UBAL3_94580002	87
UBABSL4_1305G0004	382 AAA ATPase, central domain protein		0.6712 0.034	0.0996 0.0136 0.0657 0.022		83
UBABSL4_1305G0005	88 Conserved hypothetical protein		0.3642	0.0721 0.0588 0.2497 0.058	4 0.0497 UBAL3_94580004	58
UBABSL4_2306G0001	77 Anthranilate synthase component I				UBAL3_94170010	_
UBABSL4_2306G0001	197 Anthranilate synthase component I				UBAL3_94170010	46
UBABSL4_2306G0003	164 anthranilate phosphoribosyltransferase				UBAL3_94170011	40
UBABSL4_2306G0004	270 Indole-3-glycerol-phosphate synthase				UBAL3_94170012	41
UBABSL4_2306G0005	100 Phosphoribosylanthranilate isomerase				UBAL3_94170013	
UBABSL4_3458G0001	268 acriflavin resistance protein		0.0538		UBAL3_94530074	85
UBABSL4_3458G0002	261 Putative aminomethyltransferase	0.02496	0.0387		UBAL3_94530073	67
UBABSL4_3458G0003	174 Probable secretion protein HIyD		0.0249		UBAL3_94530072	81
UBABSL4_3458G0003a	151 outer membrane efflux protein	10/554 007551 000101	0.4471 0.0096		UBAL3_94530071	76
UBABSL4_3458G0004	235 outer membrane efflux protein	1.06554 0.27551 0.23101	0.0859		UBAL3_94530071	76
UBABSL4_4822G0001	236 ATPase AAA-2 domain protein	0.01524	0.0428		UBAL3 94240025	94
UBABSL4_4822G0002	263 Rhs element Vgr protein		0.0219		UBAL3_94240024	71
UBABSL4_4822G0002a	281 Conserved hypothetical protein		0.0205		UBAL3_94240023	51
UBABSL4_4822G0003	315 pentapeptide repeat protein		0.0504		UBAL3_94240022	58
UBABSL4_4822G0004	290 pentapeptide repeat protein		0.005		UBAL3_94240022	42
UBABSL4_4897G0001	274 tryptophan synthase, beta subunit	0.01313 0.04755	0.0316		UBAL3_94170014	84
UBABSL4_4897G0001a	174 Phosphoribosylanthranilate isomerase		0.0249		UBAL3_94170013	54
UBABSL4_4897G0002	266 Indole-3-glycerol-phosphate synthase		0.0163		UBAL3_94170012	63
UBABSL4_4897G0003 UBABSL4_4897G0005	238 anthranilate phosphoribosyltransferase	0.05011			UBAL3_94170011 UBAL3_94170010	68 74
UBAB3L4_4097 G0003	65 Anthranilate synthase component I	0.03011			UBAL3_94170010	/4
UBABSL4_5872G0001a	243 protoporphyrinogen oxidase				0.009 UBAL3_92050159	61
UBABSL4_5872G0001	191 protoporphyrinogen oxidase	0.01705			UBAL3_92050159	61
UBABSL4_5872G0002	225 metallophosphoesterase				UBAL3_92050158	59
UBABSL4_5872G0003	264 Radical SAM domain protein		0.0492		UBAL3_92050157	84
UBABSL4_5872G0004	309 Glucokinase	0.03514			UBAL3_92050156	52
UBABSL4_7954G0001	127 Radical SAM domain protein				UBAL3_93200056	65
UBABSL4_7754G0001 UBABSL4_7954G0002	300 Conserved hypothetical protein		0.0529		UBAL3_93200055	74
UBABSL4_7954G0002a	89 Antibiotic biosynthesis monooxygenase	0.0366	0.2107		UBAL3_93200054	86
UBABSL4_7954G0003	526 AAA ATPase	0.0000	0.011		05/120_/0200004	00
UBABSL4_7954G0004	286 Conserved protein of unknown function				UBAL3_93200053	87
UBABSL4_8113G0001	112 General secretion pathway protein G		0.0386		UBAL3_80290008	82
UBABSL4_8113G0002	190 Putative general secretion pathway protein F		0.0076		UBAL3_80290009	74
UBABSL4_8113G0003	195 Putative general secretion pathway protein F				UBAL3_80290009	
UBABSL4_8113G0004	540 General secretion pathway protein E	0.00402	0.0107	0.0058	UBAL3_80290010	83
UBABSL4_8113G0005	370 putative general secretion pathway protein D		0.0351		UBAL3_80290011	87
UBABSL4_8582G0001	49 Conserved hypothetical protein				UBAL3_78920068	60
UBABSL4 8582G0002	105 Conserved hypothetical protein				UBAL3 78920068	52
UBABSL4_8582G0003	328 Conserved hypothetical protein			0.0096	UBAL3_78920067	48
UBABSL4_8582G0004	71 hypothetical protein				_	
UBABSL4_8582G0005	53 transposase					
UBABSL4_8896G0001	52 Heavy metal efflux pump, CzcA family	0.00000	0.05		UBAL3_95530001a	67
UBABSL4_8896G0002	360 Secretion protein HlyD	0.00999	0.0561		UBAL3_95530001	66
UBABSL4_8896G0003	297 Conserved hypothetical protein	a subunit alaba (FC / A 1 0)	0.0243		UBAL3_95530002	79
UBABSL4_8896G0004 UBABSL4_8896G0005	191 Acetyl-coenzyme A carboxylase carboxyl transferas		0.0906		UBAL3_95530003	81
UBAD3L4_0676GUUU5	47 Acetyl-coenzyme A carboxylase carboxyl transferas	e supuriii diprid (EC 6.4.1.2)	0.0307		UBAL3_95530003	77
UBABSL4 9415G0001	231 Organic solvent tolerance protein OstA				UBAL3_94170018	79
UBABSL4_9415G0002	144 Conserved protein of unknown function				UBAL3_94170019	72
UBABSL4_9415G0003	72 Conserved protein of unknown function				UBAL3_94170019	72

UBABSL4_9415G0004 UBABSL4_9415G0005	295 NAD(+) kinase (EC 2.7.1.23) 55 hypothetical protein			0.0049		UBAL3_94170020	75
UBABSL4_9462G0001 UBABSL4_9462G0002 UBABSL4_9462G0003 UBABSL4_9462G0004 UBABSL4_9462G0005	 149 geranylgeranyl reductase 250 cytochrome c biogenesis protein 185 Redoxin domain protein 284 cytochrome c assembly protein 330 ResB family protein 			0.0231 0.0312 0.0711 0.0656		UBAL3_94530015 UBAL3_94530016 UBAL3_94530017 UBAL3_94530019 UBAL3_94530020	64 91 52 98 81
UBABSL4_9480G0001 UBABSL4_9480G0002 UBABSL4_9480G0003 UBABSL4_9480G0004 UBABSL4_9480G0005	463 Glutamate dehydrogenase 112 ferredoxin 68 FeS assembly protein IscX 137 Conserved hypothetical protein 364 Putative ATP binding protein, Mrp like	0.03718 0.19763	0.23266	0.0312 0.1149		UBAL3_80420056 UBAL3_79320012 UBAL3_79320013 UBAL3_79320014 UBAL3_79320015	38 84 91 45 87
UBABSL4_9921G0001 UBABSL4_9921G0002 UBABSL4_9921G0003	128 Conserved protein of unknown function 55 hypothetical protein 45 hypothetical protein		0.04241			UBAL3_79520056	79
UBABSL4_9921G0004 UBABSL4_9921G0005	336 Ribonuclease III 155 hypothetical protein	0.08564	0.12926	0.0043 0.0093		UBAL3_79520057	74
UBABSL4_9941G0001 UBABSL4_9941G0002 UBABSL4_9941G0003 UBABSL4_9941G0004 UBABSL4_9941G0005	168 Periplasmic phosphate binding protein 377 Phosphate ABC transporter, permease protein (PstC) 221 Phosphate transport system permease protein 2 200 Phosphate import ATP-binding protein (PstB) 84 phosphate uptake regulator, PhoU		0.20086 0.16803	0.0687 0.0191		UBAL3_93200013 UBAL3_93200014 UBAL3_93200015 UBAL3_93200016 UBAL3_93200017	80 89 88 82
UBABSL4_10095G0001 UBABSL4_10095G0002 UBABSL4_10095G0003 UBABSL4_10095G0004 UBABSL4_10095G0005	337 Isocitrate dehydrogenase (NAD(+)) 116 Probable isocitrate dehydrogenase (NADP) 223 two component, sigma54 specific, transcriptional reg 74 two component, sigma54 specific, transcriptional reg 211 multi-sensor signal transduction histidine	ulator, Fis family		1.6781 1.1317 0.0194 0.039 0.0342	0.4892 0.169 0.0279	UBAL3_48660056 UBAL3_48660057 UBAL3_48660058 UBAL3_48660058 UBAL3_48660059	96 97 75 75 76
UBABSL4_10484G0001 UBABSL4_10484G0002 UBABSL4_10484G0002c UBABSL4_10484G0004 UBABSL4_10484G0005	87 Acetylornithine and succinylornithine aminotransfera 226 Acetylornithine and succinylornithine aminotransfera 208 Acetylornithine and succinylornithine aminotransfera 81 ornithine carbamoyltransferase 323 Argininosuccinate synthase	se (EC 2.6.1.11) se (EC 2.6.1.11) 0.04441	0.1201 0.03654 0.1042	0.0064		UBAL3_82700003 UBAL3_82700003 UBAL3_82700003 UBAL3_82700004 UBAL3_82700005	81 80 86
UBABSL4_10723G0001 UBABSL4_10723G0002 UBABSL4_10723G0003 UBABSL4_10723G0004 UBABSL4_10723G0005	347 Conserved hypothetical protein 267 hypothetical protein 120 transcriptional regulator, XRE family 156 hypothetical protein 255 DNA polymerase III (EC 2.7.7.7)					UBAL3_94240141 UBAL3_94240085	53 59
UBABSL4_10730G0001 UBABSL4_10730G0003 UBABSL4_10730G0005 UBABSL4_10730G0006 UBABSL4_10730G0007	254 Probable flavoprotein reductase 251 Conserved protein of unknown function 296 Dihydrolipoamide dehydrogenase 56 Dihydrolipoamide dehydrogenase (EC 1.8.1.4) 363 Conserved hypothetical protein	0.05329	0.5044 0.25954	0.1534 0.1839 0.0097 0.0119		UBAL3_80290070 UBAL3_80290071 UBAL3_80290072	94 75 67
UBABSL4_10797G0001 UBABSL4_10797G0002	57 FOG: Transposase-like 40 hypothetical protein					UBAL3_48660010	66
UBABSL4_10797G0003 UBABSL4_10797G0004 UBABSL4_10797G0005	 479 Conserved protein of unknown function 298 Conserved hypothetical protein 203 Conserved protein of unknown function 	0.02658		0.0355		UBAL3_48660052 UBAL3_48660053 UBAL3_48660054	88 88 94
UBABSL4_11008G0001 UBABSL4_11008G0002 UBABSL4_11008G0003 UBABSL4_11008G0004 UBABSL4_11008G0005	214 Conserved protein of unknown function 174 Conserved hypothetical protein 83 Conserved protein of unknown function 203 Probable ATPase, PP-loop superfamily protein 157 transposase		0.14206	0.2157 0.0249 0.0497 0.0184		UBAL3_96270005 UBAL3_96270005a UBAL3_96270006 UBAL3_96270007	71 49 72 79
UBABSL4_11387G0001	296 CRISPR-ssociated protein, Cas1		0.0515 0.2531			UBAL3_78920056	24

UBABSL4_11387G0002 UBABSL4_11387G0003 UBABSL4_11387G0004 UBABSL4_11387G0005	186 CRISPR-ssociated protein, Cas2 227 CRISPR-ssociated protein, Cas3 389 CRISPR-ssociated protein, Cas4 228 CRISPR-ssociated protein, Cas5	0.3276 0.647 0.3355 0.176 0.6265 0.722 0.334 0.704	9 1.8153 0.4942 4 1.1556 0.0824		UBAL3_78920057 UBAL3_78920058 UBAL3_78920059 UBAL3_78920060	37 36 48 45
UBABSL4_11485G0001 UBABSL4_11485G0002 UBABSL4_11485G0003 UBABSL4_11485G0004	108 Conserved protein of unknown function 461 Conserved protein of unknown function 248 Conserved hypothetical protein 55 hypothetical protein	0.00471	0.0267 0.025		UBAL3_93200122 UBAL3_93200123 UBAL3_93200124	73 76 53
UBABSL4_11485G0005	117 transcriptional regulator, LysR family		0.0493		UBAL3_93200125	59
UBABSL4_11494G0001 UBABSL4_11494G0002 UBABSL4_11494G0003 UBABSL4_11494G0004 UBABSL4_11494G0005	486 ABC1 family transporter 524 Conserved protein of unknown function 369 ATPase (AAA+ superfamily)-like 235 Cytochrome c oxidase cbb3 type, subunit I (EC 1.9.3 50 Cytochrome-c oxidase, subunit I	0.02694	0.0059 0.0165 0.0117		UBAL3_94320009 UBAL3_94320008 UBAL3_95680032 UBAL3_24060032 UBAL3_80290001	74 76 33 95 94
UBABSL4_11500G0001 UBABSL4_11500G0002 UBABSL4_11500G0003 UBABSL4_11500G0004 UBABSL4_11500G0005	134 cytochrome c, class I 457 amino-acid N-acetyltransferase 367 dTDP-glucose 4,6-dehydratase 294 glucose-1-phosphate thymidylyltransferase 59 dTDP-4-dehydrorhamnose 3,5-epimerase	0.0095 0.0355 0.00739	0.0063 0.0236 0.0343 0.0245		UBAL3_95450121 UBAL3_94170079 UBAL3_94170081 UBAL3_94170082 UBAL3_94170083	38 61 76 77 81
UBABSL4_11608G0001 UBABSL4_11608G0002 UBABSL4_11608G0003 UBABSL4_11608G0004 UBABSL4_11608G0005	351 ATPase (AAA+ superfamily)-like 560 apolipoprotein N-acyltransferase 179 Conserved protein of unknown function 153 Conserved protein of unknown function 258 DNA ligase I, ATP-dependent Dn11	0.01357 0.09043 0.06066	0.0026 0.0484 0.1697 0.0112	0.0201	UBAL3_95680032 UBAL3_94170068 UBAL3_94170069 UBAL3_94170070 UBAL3_94170071	33 53 57 67 61
UBABSL4_11676G0001	125 Resolvase helix-turn-helix domain protein				UBAL3_95530030	60
UBABSL4_11676G0002 UBABSL4_11676G0003 UBABSL4_11676G0004 UBABSL4_11676G0005	51 hypothetical protein 272 transposase 108 Conserved hypothetical protein 147 Conserved hypothetical protein			0.0233	UBAL3_48660031 UBAL3_48660029	83 76
UBABSL4_11696G0001 UBABSL4_11696G0002 UBABSL4_11696G0003 UBABSL4_11696G0004 UBABSL4_11696G0005	88 Conserved hypothetical protein 382 hypothetical protein 113 transposase 208 Putative transposase 139 hypothetical protein		0.0113	0.0151	UBAL3_80290055	35
UBABSL4_11993G0001 UBABSL4_11993G0002 UBABSL4_11993G0003 UBABSL4_11993G0004 UBABSL4_11993G0005	72 Conserved hypothetical protein 255 cytochrome B561 297 Conserved protein of unknown function 315 Conserved protein of unknown function 254 Conserved hypothetical protein	0.36459 0.42388 0.39482	0.0437		UBAL3_92050072 UBAL3_92050073 UBAL3_92050074 UBAL3_92050075	68 57 61 68
UBABSL4_12142G0001 UBABSL4_12142G0002 UBABSL4_12142G0003 UBABSL4_12142G0004 UBABSL4_12142G0005	71 aldo/keto reductase 215 Phosphoglycerate mutase 476 Cobyrinic acid a,c-diamide synthase (CbiA) 326 Precorrin-8X methylmutase CbiC/CobH 399 Fusaric acid resistance protein conserved	0.04413 0.21315	0.0406 0.0201 0.003 0.0177 0.0036		UBAL3_93670006 UBAL3_93670005 UBAL3_93670004 UBAL3_93670003 UBAL3_95320006	85 73 45 74 54
UBABSL4_12176G0001 UBABSL4_12176G0002 fRNA-Met-CAT UBABSL4_12176G0003 UBABSL4_12176G0004	358 Conserved hypothetical protein 400 Conserved hypothetical protein tRNA Met CAT 59 hypothetical protein 91 hypothetical protein		0.0121 0.0974		UBAL3_79160029 UBAL3_79160027	79 62
UBABSL4_12229G0001 UBABSL4_12229G0002 UBABSL4_12229G0003 UBABSL4_12229G0004 UBABSL4_12229G0005	252 Riboflavin kinase / FAD synthase (RibC) (EC 2.7.7.2) 138 Porphobilinogen synthase 549 Uroporphyrin-III C-methyltransferase / synthase 316 porphobilinogen deaminase 459 Glutamyl-tRNA reductase	0.18883 0.03164	0.0732 0.0091 0.0157		UBAL3_57480023 UBAL3_57480022 UBAL3_57480021 UBAL3_57480020 UBAL3_57480019	64 85 66 72 77

UBABSL4_17885G0001 UBABSL4_17885G0002	88 hypothetical protein 53 transposase					0.0328				
UBABSL4_17885G0002	286 Conserved protein of unknown function	0.03	3037			0.0504			UBAL3_94240008a	63
UBABSL4_17885G0004	400 Conserved hypothetical protein	0.01	1086			0.0289			UBAL3_94240007a	
UBABSL4_17885G0005	312 multi-sensor signal transduction histidine								UBAL3_94240007	79
UBABSL4_17901G0001	144 Probable conjugal transfer protein (TrbE)		•						UBAL3_44810039	86
UBABSL4_17901G0002	56 Conserved hypothetical protein								UBAL3_44810038	69
UBABSL4_17901G0003 UBABSL4_17901G0004	190 Probable conjugal transfer (TrbJ) 264 Probable conjugal transfer protein (TrbL)								UBAL3_44810037 UBAL3_44810036	78 82
UBABSL4_17901G0004 UBABSL4_17901G0005	203 Probable conjugal transfer profein TrbF								UBAL3_44810035a	
UBABSL4_17904G0001 UBABSL4_17904G0002	35 Cytochrome 579 159 Putative TRNA (1-methyladenosine) methyltransferase					0.5771			UBAL3_94240192a UBAL3_79520001	100 74
UBABSL4_17904G0002	271 Putative carbon-nitrogen hydrolase					0.0479			UBAL3_79520001	74
UBABSL4_17904G0004	253 Conserved protein of unknown function	0.14928 0.07	′296			0.0114			UBAL3_79520004	83
UBABSL4_17904G0005	114 Glyoxalase/bleomycin resistance protein								UBAL3_79520005	60
UBABSL4_17911G0001	49 hypothetical protein		0.6217		1.3778 1.3081	0.0294				
UBABSL4_17911G0002	169 hypothetical protein		0.3605			0.0085	0.0188	0.0186		
UBABSL4_17911G0003 UBABSL4_17911G0004	124 transcriptional regulator-like 88 Conserved protein of unknown function		0.9827 1.6188 2.077	17.22 2.4425 11.919 2.065		0.0698 0.082	0.4091 0.3963	0.0253 0.1794 0.052 0.0713 0.2529 0.149		90 88
UBABSL4_17911G0004	199 Conserved hypothetical protein		0.4592	11.717 2.063	3.3821	0.062	0.0956	0.0473 0.0172	71 UBAL3_62700037	00
UBABSL4_426G0001 UBABSL4_426G0002	216 arsenite-activated ATPase ArsA								UBAL3_95450073 UBAL3_95450074	51
UBABSL4_426G0002	50 Arsenical resistance operon trans-acting 88 hypothetical protein								UBAL3_93430074	
UBABSL4_426G0004	130 Conserved hypothetical protein									
UBABSL4 1359G0001	148 Conserved protein of unknown function					0.0292			UBAL3_79320005	56
UBABSL4_1359G0002	199 Conserved protein of unknown function					0.0072			UBAL3_79320004	67
UBABSL4_1359G0003	45 hypothetical protein								UD 410 7000000	
UBABSL4_1359G0004	287 Conserved protein of unknown function								UBAL3_79320003	
UBABSL4_2480G0001	258 diguanylate cyclase					0.0168			UBAL3_94170053	60
UBABSL4_2480G0003 UBABSL4_2480G0004	107 diguanylate cyclase 218 Lytic transglycosylase, catalytic								UBAL3_94170053 UBAL3_94170052	65 49
UBABSL4_2480G0005	47 iron-sulfur cluster assembly accessory protein								UBAL3_94170051	100
						0.110				
UBABSL4_2900G0001 UBABSL4_2900G0002	159 UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltran: 191 Putative outer membrane protein (OmpH)	sterase 0.49606 0.61204 0.23	3875			0.118 0.0982			UBAL3_95680072 UBAL3_95680073	76 79
UBABSL4_2900G0003	144 Bacterial surface antigen (D15)	0.17000 0.01201 0.20	0.0			0.0301			UBAL3_95680074	94
UBABSL4_2900G0004	312 Bacterial surface antigen (D15)	0.04338 0.04611				0.0185			UBAL3_95680074	
UBABSL4_3404G0001	72 Periplasmic molybdenum ABC transporter		<u> </u>						UBAL3_78920106	68
UBABSL4_3404G0002a	233 Molybdenum transport system, permease					0.0062			UBAL3_78920107	78
UBABSL4_3404G0002	166 Conserved hypothetical protein								UBAL3_78920109	63
UBABSL4_3404G0003	51 hypothetical protein					0.0283				
UBABSL4_3531G0001	186 outer membrane efflux protein					0.0233			UBAL3_44810096	73
UBABSL4_3531G0002 UBABSL4_3531G0003	60 secretion protein HIyD 52 hypothetical protein					0.1665			UBAL3_44810097	80
UBABSL4_3531G0004	35 hypothetical protein					0.0412				
UBABSL4_3642G0001 UBABSL4_3642G0002	103 flagellar motor switch protein FliM 119 flagellar motor switch protein FliN								UBAL3_80630058	50
UBABSL4_3642G0002	128 flagellar biosynthesis protein, FliO								2D/ (E3_00030030	50
UBABSL4_3642G0004	28 hypothetical protein									
UBABSL4_4127G0001	167 NADH dehydrogenase (quinone), chain G (EC 1.6.99.	0.04	5851			0.0777			UBAL3_60500010	59
UBABSL4_4127G0001 UBABSL4_4127G0002	57 NADH dehydrogenase (ubiquinone), H subunit	0.00	301			0.0///			UBAL3_60500010	90
UBABSL4_4127G0003	183 NADH dehydrogenase, chain I (EC 1.6.99.3)	0.22189 0.22604 0.20	1172			0.0315			UBAL3_60500008	92
UBABSL4_4127G0004	352 NADH dehydrogenase (quinone), chain L (EC 1.6.99.5	0.01533				0.0574			UBAL3_60500005	94

UBABSL4_4516G0001	185 polysaccharide deacetylase		0.0234	UBAL3_94240117	61
UBABSL4_4516G0001a	119 Conserved protein of unknown function			UBAL3_94240118	78
UBABSL4_4516G0002 UBABSL4_4516G0003	132 Conserved protein of unknown function 120 polysaccharide export protein		0.1443	UBAL3_94240118 UBAL3_94240119	47 69
0BAB3L4_4310G0003	120 polysacchanae export protein		0.1443	UBALO_/424011/	- 67
UBABSL4_5063G0001	190 diguanylate cyclase phosphodiesterase			UBAL3_79800008	62
UBABSL4_5063G0002	82 Conserved protein of unknown function		0.088	UBAL3_79800010	78
UBABSL4_5063G0003	128 Conserved protein of unknown function		0.0564	UBAL3_79800010	76
UBABSL4_5063G0004	322 Conserved protein of unknown function		0.0045	UBAL3_79800011	64
UBABSL4_6017G0001	50 NADH dehydrogenase (quinone)		0.0289	UBAL3_95680012	59
UBABSL4_6017G0002	105 Probable ferredoxin		0.055	UBAL3_95680011	62
UBABSL4_6017G0003	107 Conserved protein of unknown function			UBAL3_95680010	58
UBABSL4_6017G0004	334 Translation initiation factor, aIF-2BI/5-methylthioribos	e-1- phosphate ison 0.09752	0.0043	UBAL3_95680009	78
UBABSL4_6067G0001	263 Conserved hypothetical protein			UBAL3_74420016	39
UBABSL4_6067G0002	206 hypothetical protein		0.021	0BAL5_74420010	37
UBABSL4_6067G0003	208 Putative non-canonical purine NTP pyrophosphatase	, rdgB/HAM1 family 0.01044	0.0347	UBAL3_74420018	59
UBABSL4_6067G0004	49 hypothetical protein				
LID A DCL 4 (1.40,000)	221 Canage and by matheating the state of		0.00/0	0.0707 0.0004 0.0051 0.007 0.0140 HB.412 0500007	4.4
UBABSL4_6142G0001 UBABSL4_6142G0002	231 Conserved hypothetical protein 67 hypothetical protein		0.0062	0.0686 0.0224 0.0951 0.037 0.0142 UBAL3_95390007	44
UBABSL4_6142G0002	44 hypothetical protein			0.0721 0.0389	
UBABSL4_6142G0004	416 FOG: Transposase-like	0.0732	0.3852 0.059	0.1829 0.0373 0.0906 0.037 0.0053 UBAL3_48660010	57
UBABSL4_6593G0001	52 Conserved hypothetical protein		0.071	UBAL3_95680117	69
UBABSL4_6593G0002 UBABSL4_6593G0003	303 3-hydroxyisobutyrate dehydrogenase 165 hypothetical protein		0.0714	UBAL3_95680118	64
UBABSL4_6593G0004	336 Putative permease		0.0086	UBAL3_95680120	76
05/15021_00/000001	oo i oranio pornioaso		0.0000	05/125_/0000120	, ,
UBABSL4_6942G0001	115 Conserved hypothetical protein			UBAL3_93200091	47
UBABSL4_6942G0002	325 Conserved hypothetical protein		0.0044	UBAL3_93200092	85
UBABSL4_6942G0003 UBABSL4_6942G0004	147 Conserved hypothetical protein 186 thiazole biosynthesis family protein ThiG	0.01934 0.12842	0.0931	UBAL3_95450136 UBAL3_93200094	68 89
0BAB3L4_0742G0004	iniazore biosyninesis family profesii filie	0.01734 0.12042	0.0731	0BAL5_73200074	07
UBABSL4_7131G0001	241 cell shape determining protein, MreB/Mrl family	0.08209 0.01802	0.1018	UBAL3_94530045	95
UBABSL4_7131G0002	99 Conserved protein of unknown function		0.0291	UBAL3_94530046	54
UBABSL4_7131G0003	228 Ribulose-phosphate 3-epimerase		0.0443	UBAL3_94530047	74
UBABSL4_7131G0004	252 peptidase M48		0.1088	UBAL3_94530048	85
UBABSL4_7671G0001	202 Putative peptidyl-prolyl cis-trans isomerase			UBAL3_79520065	56
UBABSL4_7671G0002	155 Probable peptidil-prolyl cis-trans isomerase			UBAL3_79520066	70
UBABSL4_7671G0003	103 Probable peptidil-prolyl cis-trans isomerase	0.03492		UBAL3_79520066	69
UBABSL4_7671G0004	291 transcription-repair coupling factor		0.0099	UBAL3_79520067	74
UBABSL4 8194G0001	277 Probable cytochrome b/b6, C-terminal	0.12216 0.11038 0.03528	0.2396	UBAL3_94170024	97
UBABSL4_8194G0001	72 Conserved protein of unknown function	0.12216 0.11036 0.03326	0.2376	UBAL3_94170025	94
UBABSL4_8194G0002a	233 Probable cytochrome c, class I		0.3034	UBAL3_94170026	82
UBABSL4_8194G0003	225 transposase		0.0577		
LIDADOLA OCACCOCC	107 HTD when and a break had a little of the	0.0100/ 0.00007		110.110.0700000	^ ·
UBABSL4_8268G0001 UBABSL4_8268G0002	197 UTP-glucose-1-phosphate uridylyltransferase GalU 331 thiamine-monophosphate kinase	0.01826 0.03307	0.022 0.0305	UBAL3_94320058 UBAL3_94320057	84 56
UBABSL4_8268G0002a	152 Conserved hypothetical protein		0.0095	UBAL3_94320056	65
UBABSL4_8268G0003	214 OmpA family protein		3133.3	UBAL3_94320055	58
UBABSL4_8752G0001	132 hypothetical protein				
UBABSL4_8752G0002 UBABSL4_8752G0004	126 hypothetical protein 191 Putative phosphatidylethanolamine binding protein		0.1485 0.0453	UBAL3 94530001a	72
UBABSL4_8752G0004 UBABSL4_8752G0005	145 4-hydroxybenzoate polyprenyl transferase		0.0453	UBAL3_94530001d UBAL3_94530001	73 67
	, and any and profit in an arrangement			55, 125_, 1000001	<u> </u>
UBABSL4_8800G0001	234 Precorrin-3B methylase (EC 2.1.1.131)	0.17168	0.0308	UBAL3_79520031	69
UBABSL4_8800G0002 UBABSL4_8800G0003	57 Precorrin-3B methylase (EC 2.1.1.131) 181 cob(I)alamin adenosyltransferase	0.07198	0.0319	UBAL3_79520031 UBAL3_79520032	80 81

UBABSL4_8800G0004	177 <mark>peptide deformylase</mark>	0.01227	0.0489		UBAL3_79520033	85
UBABSL4_9000G0001 UBABSL4_9000G0002 UBABSL4_9000G0003 UBABSL4_9000G0004	86 metal dependent phosphohydrolase 125 Conserved protein of unknown function 181 Conserved hypothetical protein 310 Glycine dehydrogenase (decarboxylating)	0.0174 0.09106	0.0335		UBAL3_80630078 UBAL3_80630079 UBAL3_80630080 UBAL3_80630081	78 53 46 80
UBABSL4_9110G0001 UBABSL4_9110G0002 UBABSL4_9110G0003 UBABSL4_9110G0004	535 acriflavin resistance protein 138 Secretion protein (HIyD) 204 Secretion protein (HIyD) 103 outer membrane efflux protein	0.78846 0.36668 0.29515	0.0027		UBAL3_95320052 UBAL3_95320051 UBAL3_95320051 UBAL3_95320050	81 66 66 80
UBABSL4_9171G0001 UBABSL4_9171G0002 UBABSL4_9171G0003 UBABSL4_9171G0004	35 Conserved hypothetical protein 152 Conserved protein of unknown function 229 methyltransferase 150 peptidase M16 domain protein		0.0412 0.2752 0.3499 0.0252 0.0096	0.0137	UBAL3_74420031 UBAL3_74420030	63 55
UBABSL4_9271G0001 UBABSL4_9271G0002 UBABSL4_9271G0003 UBABSL4_9271G0004	120 Acetyl-CoA synthetase (EC 6.2.1.1) 136 Putative glyoxalase (GloA) 163 Conserved hypothetical protein 243 Conserved hypothetical protein	0.0181	0.0106 0.0059		UBAL3_93200090 UBAL3_93200089 UBAL3_95450090	87 71 53
UBABSL4_9320G0001 UBABSL4_9320G0002 UBABSL4_9320G0003 UBABSL4_9320G0004	138 Conserved protein of unknown function 370 Conserved hypothetical protein 299 Conserved hypothetical protein 65 phage integrase family protein				UBAL3_95680101 UBAL3_95680102 UBAL3_95680102 UBAL3_95680103	61 49 49 53
UBABSL4_9385G0001 UBABSL4_9385G0002 UBABSL4_9385G0003 UBABSL4_9385G0004	134 Conserved protein of unknown function 100 Conserved hypothetical protein 202 Conserved hypothetical protein 148 transposase	0.03241	0.05 0.3022		UBAL3_94170005 UBAL3_94170004 UBAL3_94170003	68 75 94
UBABSL4_9449G0001 UBABSL4_9449G0002 UBABSL4_9449G0003 UBABSL4_9449G0004	286 Conserved protein of unknown function 222 Conserved hypothetical protein 461 Conserved hypothetical protein 99 Conserved hypothetical protein		0.0202 0.0195 0.0156 0.0291		UBAL3_94240015 UBAL3_94240016 UBAL3_94240017 UBAL3_94240018	84 67 88 79
UBABSL4_9572G0001 UBABSL4_9572G0002 UBABSL4_9572G0003 UBABSL4_9572G0004	26 hypothetical protein 394 glycosyl transferase, group 1 260 polysaccharide deacetylase 252 O-antigen polymerase		0.0146 0.0277 0.0114		UBAL3_94240115 UBAL3_94240114 UBAL3_94240113	82 78 80
UBABSL4_9813G0001 UBABSL4_9813G0002 UBABSL4_9813G0003 UBABSL4_9813G0004	46 hypothetical protein 361 multicopper oxidase 296 Putative NAD-binding 6-phosphogluconate dehydro 94 Putative type IV prepilin peptidase	genase			UBAL3_92050191 UBAL3_92050192	69 60
UBABSL4_10241G0001 UBABSL4_10241G0002 UBABSL4_10241G0003 UBABSL4_10241G0004	589 DNA polymerase B region 286 Putative methyltransferase 51 hypothetical protein 262 Putative methyltransferase	0.01658	0.0555 0.1414 0.1101		UBAL3_93200072 UBAL3_92050119 UBAL3_92050117	62 66
UBABSL4_10295G0001 UBABSL4_10295G0002 UBABSL4_10295G0003 UBABSL4_10295G0004	280 Conserved hypothetical protein 102 Conserved hypothetical protein 113 Conserved hypothetical protein 411 Conserved hypothetical protein		0.	0.0226 0.037 0.1345 0.1015 0.0923 0.0281 0.1667 0.0151 0.0926 0.0756 0.084 0.0083	UBAL3_95390008 UBAL3_95390008 UBAL3_95390007 UBAL3_95390007	82 73 62 94
UBABSL4_10326G0001 UBABSL4_10326G0002 UBABSL4_10326G0003 UBABSL4_10326G0004	185 hypothetical protein 244 Conserved protein of unknown function 147 thioredoxin 316 Aminopeptidase N (EC 3.4.11.2)	0.01138 0.0378	0.1794 0.0296 0.0046	0.0093 0.0	UBAL3_92050076 UBAL3_92050077 UBAL3_92050078	66 55 75
UBABSL4_10355G0001 UBABSL4_10355G0002	220 Putative mechanosensitive ion channel (MscS) 95 probable DNA binding protein		0.0262			

UBABSL4_10355G0003 UBABSL4_10355G0004	87 hypothetical protein 354 <mark>Vesicle-fusing ATPase</mark>	0.01016	0.1161 0.0571	UBAL3_92050098 73
UBABSL4_10381G0001 UBABSL4_10381G0002	408 isoleucyl-tRNA synthetase 555 isoleucyl-tRNA synthetase		0.0177 0.0234	UBAL3_79520011 53 UBAL3_79520011
tRNA-Val-CAC UBABSL4_10381G0003	tRNA Val CAC 100 DNA polymerase III, epsilon subunit			UBAL3_79520016 35
UBABSL4_10473G0001 UBABSL4_10473G0002 UBABSL4_10473G0003 UBABSL4_10473G0004	464 Putative adenylylsulfate reductase, subunit A 116 Probable adenylylsulfate reductase, subunit B 402 sulfate adenylyltransferase 65 hypothetical protein (transcriptional regulator)	0.04914 0.05816 0.17015	0.028 0.0249 0.0754 0.1776	UBAL3_79160037 77 UBAL3_79160036 86 UBAL3_79160035 87
UBABSL4_10576G0001 UBABSL4_10576G0002 UBABSL4_10576G0003 UBABSL4_10576G0004	98 Conserved hypothetical protein 293 Putative ATPase, AAA family 337 Conserved hypothetical protein 203 Conserved hypothetical protein		0.0098	UBAL3_95450061 86 UBAL3_95680106 68 UBAL3_95680107 62 UBAL3_95680108 68
UBABSL4_10595G0001 UBABSL4_10595G0002 UBABSL4_10595G0003 UBABSL4_10595G0004	90 Conserved hypothetical protein 147 Conserved hypothetical protein 53 Conserved hypothetical protein 189 IstB-like ATP-binding protein	0.34257 0.47107 10.557	7 2.3365 2.5766 5.4484 6.4296 6.1047 3.3433	0.4227 0.038 0.0243 UBAL3_96270025 59 0.2157 0.0352 0.1708 0.0466 0.0149 UBAL3_96270024 86 0.1196 0.1954 0.3554 0.0323 0.0206 UBAL3_96270023 98 9.7131 17.427 8.6867 12.969 6.1884
UBABSL4_10760G0001 UBABSL4_10760G0002 UBABSL4_10760G0003 UBABSL4_10760G0004	204 Acetohydroxy acid isomeroreductase 169 acetolactate synthase, small subunit 533 acetolactate synthase, large subunit, 67 acetolactate synthase, large subunit,	0.03193 0.10922 0.02539 0.11472 0.12222	0.0141 0.0341 0.0541	UBAL3_94240042 92 UBAL3_94240043 86 UBAL3_94240044 87 UBAL3_94240044 97
UBABSL4_10769G0001 UBABSL4_10769G0002 UBABSL4_10769G0003 UBABSL4_10769G0004	487 Probable conjugal transfer protein (TrbE) 103 Probable conjugal transfer protein (TrbD) 101 Conserved hypothetical protein 148 Putative conjugal transfer protein (TrbB)			UBAL3_44810040 78 UBAL3_44810041 72 UBAL3_44810042 65 UBAL3_44810043 87
UBABSL4_10788G0001 UBABSL4_10788G0002 UBABSL4_10788G0003 UBABSL4_10788G0004	554 periplasmic sensor signal transduction histidine kinase 176 Probable hexapeptide transferase family protein 243 Conserved protein of unknown function 21 hypothetical protein		0.0078 0.0246 0.0059	UBAL3_93200046 63 UBAL3_93200045 82 UBAL3_93200044 66
UBABSL4_10802G0001 UBABSL4_10802G0002 UBABSL4_10802G0003 UBABSL4_10802G0004	246 UDP-glucose 6-dehydrogenase (EC 1.1.1.22) 483 glucosaminefructose-6-phosphate aminotransferas 76 hypothetical protein 364 Putative endonuclease	0.0662 e [isomerizing] (EC: 0.02248	0.0445 0.0388	UBAL3_94240095 89 UBAL3_94240096 85 UBAL3_94530056 74
UBABSL4_10971G0001 UBABSL4_10971G0002 UBABSL4_10971G0003 UBABSL4_10971G0005	62 Conserved hypothetical protein 218 3-isopropylmalate dehydratase, small subunit 468 3-isopropylmalate dehydratase, large subunit 257 transcriptional regulator, LysR family	0.10957 0.04227 0.38744	0.0132 0.0493	UBAL3_94170075 71 UBAL3_94170076 79 UBAL3_94170077 82 UBAL3_94170078 63
UBABSL4_11269G0001 UBABSL4_11269G0002 UBABSL4_11269G0003 UBABSL4_11269G0004	257 Probable lipopolysaccharide heptosyltransferase II 343 Putative heptosyltransferase family protein 245 polysaccharide deacetylase 310 glycosyl transferase, family 1		0.0084 0.014	UBAL3_95680058 55 UBAL3_95680057 66 UBAL3_95680056 65 UBAL3_95680055 63
UBABSL4_11296G0001 UBABSL4_11296G0002 UBABSL4_11296G0003 UBABSL4_11296G0004	 cytidylate kinase 3-phosphoshikimate 1-carboxyvinyltransferase Prephenate dehydrogenase phospho-2-dehydro-3-deoxyheptonate aldolase 	0.00965 0.08501 0.06946 0.11719 0.51385 0.90714	0.0385 0.0194 0.0146 0.0625	UBAL3_95320017 65 UBAL3_95320016 73 UBAL3_95320015 61 UBAL3_95320014 93
UBABSL4_11309G0001 UBABSL4_11309G0002 UBABSL4_11309G0003 UBABSL4_11309G0004	258 glycosyl transferase, group 1 393 glycosyl transferase, group 1 267 polysaccharide deacetylase 269 protein tyrosine phosphatase		0.0037 0.0378 0.0054	UBAL3_94240109 76 UBAL3_94240110 86 UBAL3_94240111 70 UBAL3_94240112 58
UBABSL4_11790G0001	710 Putative helicase, Snf2 family			UBAL3_95950014 36

UBABSL4_11790G0002 UBABSL4_11790G0003 UBABSL4_11790G0004	149 Conserved protein of unknown function 223 transcriptional repressor, LexA family 373 putative chemotaxis phosphatase, CheZ	0.03375 0.06113	0.0097 0.0129 0.0812	UBAL3_95950013 75 UBAL3_95950012 37 UBAL3_95950011 59
UBABSL4_12069G0001 UBABSL4_12069G0002 UBABSL4_12069G0003 UBABSL4_12069G0004	553 [Nife] hydrogenase large subunit HydB 369 [Nife] hydrogenase small subunit HydA 197 thymidylate kinase 221 Thymidylate kinase	0.01951	0.0496 0.0274 0.022	UBAL3_94530007 76 UBAL3_94530008 87
rRNA-16\$ tRNA-lle-GAT tRNA-Ala-TGC rRNA-23\$	16S rRNA tRNA IIe GAT tRNA Ala TGC 23S rRNA			
UBABSL4_13359G0001 UBABSL4_13359G0002 UBABSL4_13359G0003 UBABSL4_13359G0004	264 Conserved hypothetical protein 185 Deoxyribonuclease, TatD family 93 methionyl-tRNA synthetase 294 hypothetical protein		0.0219 0.0156 0.0294	UBAL3_94240088 74 UBAL3_94240087 84
UBABSL4_17890G0001 UBABSL4_17890G0002 UBABSL4_17890G0003 UBABSL4_17890G0004	211 Putative endonuclease III 657 glycoside hydrolase, family 15 591 diguanylate cyclase/phosphodiesterase 166 transposase		0.0154 0.0024	UBAL3_95680141 35 UBAL3_95950017 68 UBAL3_74420053 45
UBABSL4_17891G0001 UBABSL4_17891G0002 UBABSL4_17891G0003 UBABSL4_17891G0004	 239 methyl-accepting chemotaxis sensory transducer 159 Thiamine biosynthesis protein (ThiC) 286 Probably 5-methyltetrahydrofolatehomocysteine 266 5-methyltetrahydrofolatehomocysteine methyltra 		0.0664 0.1542 0.0101	UBAL3_94240159 41 UBAL3_80290068 87 UBAL3_80290067 83 UBAL3_80290066 83
UBABSL4_2740G0001 UBABSL4_2740G0002 UBABSL4_2740G0003	112 Conserved hypothetical protein 191 N-acetyl-gamma-glutamyl-phosphate reductase 259 arginine biosynthesis bifunctional protein ArgJ		0.0245	0.0098 0.0164 0.0458 UBAL3_94530032 42 0.0121 0.0211 UBAL3_94530029 41
UBABSL4_3307G0001 UBABSL4_3307G0002 UBABSL4_3307G0003	130 Conserved hypothetical protein 152 Conserved hypothetical protein 472 hypothetical protein		0.0031	UBAL3_95680111 66 UBAL3_95680112 75
UBABSL4_3660G0001 UBABSL4_3660G0002 UBABSL4_3660G0003	194 Conserved hypothetical protein 180 Conserved protein of unknown function 463 Conserved protein of unknown function			UBAL3_80290077 52 UBAL3_80290076 86 UBAL3_80290076
UBABSL4_3690G0001 UBABSL4_3690G0002 UBABSL4_3690G0003	40 hypothetical protein 235 TPR-domain containing protein 87 TPR-domain containing protein		0.1412 0.1327	UBAL3_79520009 80 UBAL3_79520009 83
UBABSL4_3990G0001 UBABSL4_3990G0002 UBABSL4_3990G0003	257 cobyric acid synthase CobQ 180 cobalamin biosynthesis protein CobD/CbiB 320 Putative L-threonine-O-3-phosphate decarboxylase	e		UBAL3_95450140 52 UBAL3_95450139 61 UBAL3_95450138 54
UBABSL4_4294G0001 UBABSL4_4294G0002 UBABSL4_4294G0003	106 Conserved hypothetical protein 106 Putative iron-sulfur cofactor synthesis protein (NifZ) 82 Conserved hypothetical protein			UBAL3_78920092 72 UBAL3_78920093 86 UBAL3_78920094 68
UBABSL4_4393G0001 UBABSL4_4393G0002 UBABSL4_4393G0003	211 Putative hydrogenase-4 subunit (HyfF) 86 Probable hydrogenase-4 membrane component (231 respiratory-chain NADH dehydrogenase, subunit 1			UBAL3_79520044 56 UBAL3_79520045 65
UBABSL4_4489G0001 UBABSL4_4489G0002 UBABSL4_4489G0003	197 Conserved protein of unknown function 119 Conserved hypothetical protein 200 3-dehydroquinate synthase			UBAL3_44810079 55 UBAL3_44810080 69 UBAL3_44810082 64
UBABSL4_6289G0001 UBABSL4_6289G0002 UBABSL4_6289G0003	183 UDP-3-0-acyl N-acetylglucosamine deacetylase 103 ferredoxin 199 Conserved protein of unknown function		0.0315 0.029	UBAL3_79520053 68 UBAL3_79520054 65 UBAL3_79520055 60

UBABSL4_7181G0001 UBABSL4_7181G0002 UBABSL4_7181G0003	158 phosphoribosylaminoimidazole-succinocarboxamide 101 phosphoribosylformylglycinamidine synthase, PurS 400 Conserved protein of unknown function	synthase 0.08246 0.30271 0.07525	0.0091 0.0143	UBAL3_96150015 83 UBAL3_96150016 81 UBAL3_96150017 58
UBABSL4_7408G0001 UBABSL4_7408G0002 UBABSL4_7408G0003	218 heat-inducible transcription repressor HrcA 168 Putative GrpE protein 74 hypothetical protein			UBAL3_80420055 27 UBAL3_80420057 43
UBABSL4_7482G0001 UBABSL4_7482G0002	145 Phosphoglycerate kinase	0.56791	0.1463	UBAL3_94530104 85 UBAL3_94530103 86
UBABSL4_7482G0003	231 Phosphoglycerate kinase	0.14649 0.26471 0.46532	0.0687	UBAL3_94530103 91
UBABSL4_7641G0001 tRNA-Met-CAT	147 Conserved protein of unknown function tRNA Met CAT		0.0196	UBAL3_94240172 66
UBABSL4_7641G0002	191 RNA polymerase, sigma 70 subunit, RpoD	0.12241 0.01705	0.0453	UBAL3_94240173 96
UBABSL4_7680G0001 UBABSL4_7680G0002 UBABSL4_7680G0003	89 Conserved hypothetical protein 181 Queuosine biosynthesis protein 155 Conserved protein of unknown function		0.0324	UBAL3_94240035 77 UBAL3_94240034 68 UBAL3_95530042 91
UBABSL4_7894G0001 UBABSL4_7894G0002 UBABSL4_7894G0003	99 aspartate-semialdehyde dehydrogenase 300 3-isopropylmalate dehydrogenase 316 3-isopropylmalate dehydrogenase	0.0987 0.09024 0.09592 0.33296	0.0192 0.0548	UBAL3_94240037 82 UBAL3_94240038 87 UBAL3_94240038 87
UBABSL4_8037G0001 UBABSL4_8037G0002 UBABSL4_8037G0004	109 signal peptidase I 240 Carbohydrate kinase, PfkB 261 3-deoxy-D-manno-octulosonate	0.12739 0.27144 0.05513 0.04992	0.024	UBAL3_95950022 75 UBAL3_95950023 74 UBAL3_95950024 73
UBABSL4_9348G0001 UBABSL4_9348G0002 UBABSL4_9348G0003	156 Phage integrase343 flagellar motor switch protein FliM65 Carboxymethylenebutenolidase	0.01049 0.0095	0.0277 0.0084	UBAL3_94170001a 27 UBAL3_80630007 89 UBAL3_80630008 54
UBABSL4_9408G0001 UBABSL4_9408G0002 UBABSL4_9408G0003	103 Conserved hypothetical protein521 Phosphoenolpyruvate carboxylase63 Conserved hypothetical protein	0.15879 0.22924	0.0249	UBAL3_79520052 87 UBAL3_79520051 88 UBAL3_79520050 82
UBABSL4_9434G0001 UBABSL4_9434G0002 UBABSL4_9434G0003	231 ammonium transporter 113 nitrogen regulatory protein P-II 69 transcriptional regulator AbrB family	0.09549 0.81671	0.1499 0.1277	UBAL3_92050069 89 UBAL3_92050070 84
UBABSL4_9683G0001 UBABSL4_9683G0002 UBABSL4_9683G0003	223 glutamate racemase 151 heat shock protein Hsp20 108 pseudouridine synthase	0.53783	1.0414	UBAL3_74420023 75 UBAL3_74420024 75 UBAL3_74420025 49
UBABSL4_9970G0001 UBABSL4_9970G0002 UBABSL4_9970G0003	267 oligopeptide/dipeptide ABC transporter, ATPase 265 Phosphomethylpyrimidine kinase 164 peptidase M23B		0.0432 0.044	UBAL3_93200099 70 UBAL3_93200097 56 UBAL3_93200096 78
UBABSL4_9975G0001 UBABSL4_9975G0002 UBABSL4_9975G0003	99 Conserved protein of unknown function 330 DNA mismatch repair protein MutS 420 DNA mismatch repair protein MutS	0.0109	0.0146	UBAL3_92050213 58 UBAL3_92050212 78 UBAL3_92050212 63
UBABSL4_10073G0001 UBABSL4_10073G0002 UBABSL4_10073G0003	111 Conserved protein of unknown function 467 diguanylate cyclase phosphodiesterase 296 diguanylate cyclase phosphodiesterase		0.013 0.0463 0.0146	UBAL3_79800007 45 UBAL3_79800008 67 UBAL3_79800008 67
UBABSL4_10187G0001 UBABSL4_10187G0002 UBABSL4_10187G0003	422 Conserved protein of unknown function 51 hypothetical protein 403 DNA repair protein RecN		0.0034	UBAL3_44810113 70 UBAL3_44810116 60
UBABSL4_10346G0001 UBABSL4_10346G0002 UBABSL4_10346G0003	112 2-oxoglutarate dehydrogenase complex, dihydrolipoa 568 2-oxoglutarate dehydrogenase complex, dehydrogen 134 Conserved hypothetical protein		0.0644 0.066 0.1066 0.4754 0.395 0.1626	0.8493 1.2947 1.0651 0.8253 0.732 UBAL3_80420069 95 0.9378 1.5956 1.3209 1.4495 1.4203 UBAL3_80420070 100

UBABSL4_10523G0001 UBABSL4_10523G0002 UBABSL4_10523G0003	601 Peptidase S1C, Do 214 Probable holliday junction DNA helicase (RuvA) 204 Holliday junction DNA helicase RuvB	0.54051 0.2334	0.06684 0.01015			0.1008 0.0202 0.0424			UBAL3_93200048 UBAL3_93200050 UBAL3_93200051	86 66 87
UBABSL4_11228G0001 UBABSL4_11228G0002 UBABSL4_11228G0003	169 Conserved hypothetical protein 84 hypothetical protein 424 Aminopeptidase N (EC 3.4.11.2)		0.06146			0.0939 0.0515 0.0204	0.0306	0.0405 0.0065	UBAL3_92050078	55
UBABSL4_11254G0001 UBABSL4_11254G0002 UBABSL4_11254G0003	124 amidophosphoribosyltransferase 742 phosphoribosylformylglycinamidine synthase II 236 phosphoribosylformylglycinamidine synthase I		0.03658			0.0233 0.0078 0.0917			UBAL3_95320044 UBAL3_95320045 UBAL3_95320046	77 75 66
UBABSL4_11334G0001 UBABSL4_11334G0002 UBABSL4_11334G0003	597 <mark>deoxyxylulose-5-phosphate synthase</mark> 184 Probable hemolysin 126 NAD-dependent epimerase/dehydratase	0.00603	3 0.04365			0.0169 0.0078 0.0114			UBAL3_60500022 UBAL3_60500021 UBAL3_60500020	83 60 63
UBABSL4_11454G0001 UBABSL4_11454G0002 UBABSL4_11454G0003	360 peptidase C14, caspase catalytic subunit p20 235 peptidase C14, caspase catalytic subunit p20 115 Cellulose synthase catalytic subunit (UDP-forming)								UBAL3_95450007 UBAL3_95450007	31 34
UBABSL4_11504G0001 UBABSL4_11504G0002 UBABSL4_11504G0003	92 Dihydrolipoamide dehydrogenase (EC 1.8.1.4) 470 glutamine synthetase, type I 391 transcriptional regulator, NifA, Fis Family	0.27359 0.5280	5 0.69303 0.0361			0.1842 0.0037			UBAL3_94170054 UBAL3_94170056 UBAL3_94170057	63 90 85
UBABSL4_11710G0001 UBABSL4_11710G0002 UBABSL4_11710G0003	90 hypothetical protein 476 Conserved protein of unknown function 245 ammonium transporter	2.6445 0.6876	5 0.49725			0.0697 0.0353	0.0133 0.0109 0.006	6	UBAL3_92050068 UBAL3_92050069	88 96
UBABSL4_12343G0001 UBABSL4_12343G0002 UBABSL4_12343G0003	134 Transposase-like 417 transposase 87 hypothetical protein					0.3494	0.0124		UBAL3_94240057	
UBABSL4_12576G0001 UBABSL4_12576G0002 UBABSL4_12576G0003	252 Conserved hypothetical protein228 Conserved protein of unknown function233 transposase		0.15844			0.0124			UBAL3_80290017 UBAL3_80290016 UBAL3_93670016	55 74 46
UBABSL4_12683G0001 UBABSL4_12683G0002 UBABSL4_12683G0003	408 Dihydrolipoamide dehydrogenase 447 Conserved hypothetical protein 53 hypothetical protein		0.01064 0.01214			0.0389			UBAL3_79160026 UBAL3_95950035	58 56
UBABSL4_17877G0001 UBABSL4_17877G0002 UBABSL4_17877G0003	95 hypothetical protein 432 Adenylosuccinate synthase 83 Conserved protein of unknown function	0.0874	3 0.09551		0.1563	0.1069			UBAL3_94320006 UBAL3_94320007	85 46
UBABSL4_17899G0001 UBABSL4_17899G0002 UBABSL4_17899G0003	136 Homoserine dehydrogenase 93 threonine synthase 187 Probable phosphoglycerate mutase					0.0212			UBAL3_95450115 UBAL3_95450114 UBAL3_95450113	77 80 42
UBABSL4_684G0001 UBABSL4_684G0002	213 NAD-dependent epimerase/dehydratase 288 Conserved protein of unknown function					0.0068 0.02			UBAL3_95450095 UBAL3_95450093	75 62
UBABSL4_802G0001 UBABSL4_802G0002	314 Putative filamentous haemagglutinin family protein 303 Putative filamentous haemagglutinin family protein			0.097	0.1021	0.0276 0.019	0.1919 0.2144 0.0 0.0732 0.0342 0.051			97 44
UBABSL4_2328G0001 UBABSL4_2328G0002	182 Conserved protein of unknown function 239 phosphoglucomutase, alpha-D-glucose		0.00909			0.5469 0.0362			UBAL3_96150002 UBAL3_96150004	70 68
UBABSL4_3153G0001 UBABSL4_3153G0002	123 Probable rieske iron-sulfur family protein 206 Cytochrome b/b6, N-terminal domain					0.0938 0.042			UBAL3_92050216 UBAL3_92050217	90 91
UBABSL4_4391G0001 UBABSL4_4391G0002	145 peptidase M23B 113 preprotein translocase, SecA subunit					0.0099 0.0511			UBAL3_60500018 UBAL3_60500017	73 77

UBABSL4_4579G0001 UBABSL4_4579G0002	72 Probable N-acetyltransferase family protein 204 peptide chain release factor 2		0.03193			0.0212			UBAL3_94170066 UBAL3_94170067	57 89
UBABSL4_4962G0001 UBABSL4_4962G0002	130 Putative sulfite synthesis pathway protein (CysQ) 295 Conserved hypothetical protein					0.0111 0.0098			UBAL3_78920010 UBAL3_78920011	64 55
UBABSL4_6076G0001 UBABSL4_6076G0002	103 riboflavin biosynthesis protein RibD (EC:3.5.4.26 1.1.1.1 195 riboflavin synthase, alpha subunit	193)							UBAL3_95450154	44
UBABSL4_6180G0001 UBABSL4_6180G0002	181 Polyribonucleotide nucleotidyltransferase 44 Ribosomal protein \$15								UBAL3_92050205 UBAL3_92050204	50
UBABSL4_6185G0001 UBABSL4_6185G0002	244 Conserved hypothetical protein 228 Conserved protein of unknown function								UBAL3_95680069	41
UBABSL4_7122G0001 UBABSL4_7122G0002	184 NADH dehydrogenase (quinone) F subunit 189 <mark>Putative NADH dehydrogenase (ubiquinone), E subut</mark>		319 0.15932 644 0.22979			0.149 0.0687			UBAL3_60500011 UBAL3_60500012	91 85
UBABSL4_7607G0001 UBABSL4_7607G0002	321 putative aconitate hydratase 213 hypothetical protein	1.1174 1.266	521 1.02486			0.1528 0.1151			UBAL3_92050122	95
UBABSL4_7720G0001 UBABSL4_7720G0002	232 Cystathionine gamma-synthase 50 transposase		0.06552			0.0062 0.1731			UBAL3_92050065	68
UBABSL4_8065G0001 UBABSL4_8065G0002	323 Putative general secretion pathway protein K 322 Conserved protein of unknown function					0.009			UBAL3_80290004 UBAL3_80290003	79 70
UBABSL4_8108G0001 UBABSL4_8108G0002	204 Conserved hypothetical protein 37 hypothetical protein			0.0747		0.0786	0.0933	0.0848	UBAL3_95390017	84
UBABSL4_8247G0001 UBABSL4_8247G0002	128 Conserved protein of unknown function 231 Conserved protein of unknown function								UBAL3_92050231 UBAL3_92050232	70 53
UBABSL4_8572G0001 UBABSL4_8572G0002	187 UDP-glucose 4-epimerase (EC 5.1.3.2) 162 Conserved protein of unknown function		0.0987			0.0077 0.1069			UBAL3_94240092 UBAL3_94240093	92 55
UBABSL4_9030G0001 UBABSL4_9030G0002	59 hypothetical protein 617 GTP-binding protein					0.0468			UBAL3_94240168	84
UBABSL4_9383G0001 UBABSL4_9383G0002	496 UDP-N-acetylmuramoylalanineD-glutamate ligase 356 phospho-N-acetylmuramoyl-pentapeptide-transfera		0.01532			0.0081			UBAL3_92050139 UBAL3_92050138	62 83
UBABSL4_9559G0001 UBABSL4_9559G0002	930 NADH dehydrogenase, subunit F (EC 1.6.99.5) 247 NADH dehydrogenase, subunit F (EC 1.6.99.5)	0.054	0.13426 0.02637			0.1427 0.0584			UBAL3_95680142 UBAL3_95680142	94
UBABSL4_9818G0001 UBABSL4_9818G0002	277 Conserved protein of unknown function 431 transposase					0.0156 0.0703			UBAL3_94530059	46
UBABSL4_9882G0001 UBABSL4_9882G0002	metal dependent phosphohydrolase 488 glycosyl transferase, family protein	0.095	525 0.17927 0.02892			0.0135 0.0059			UBAL3_79160020 UBAL3_79160019	77 51
UBABSL4_11135G0001 UBABSL4_11135G0002	375 Transcription termination factor (NusA) 753 translation initiation factor IF-2	0.11 0.06291 0.097	199 0.14477 792 0.17014			0.1885 0.0632			UBAL3_92050199 UBAL3_92050200	85 77
UBABSL4_11310G0001 UBABSL4_11310G0002	884 Conserved protein of unknown function 117 nitrogen regulatory protein P-II					0.0033			UBAL3_74420059 UBAL3_74420058	68 89
UBABSL4_17913G0001 UBABSL4_17913G0002	94 CRISPR-ssociated protein, Cas2 307 Conserved hypothetical protein			0.3241 0.2481	0.797 0.8541 0.1973	0.1705 1.3049 0.0047		0.0056 0.007	UBAL3_78920062	67
UBABSL4_2192G0001	282 Probable TPR-domain containing protein								UBAL3_94240129	71
UBAB\$L4_4241G0001	296 Conserved protein of unknown function	0.09145 0.097	721			0.078			UBAL3_69480020	69

 UBABSL4_10441G0001
 348 Organic solvent tolerance protein OstA
 0.0083
 UBAL3_94170018
 75

 UBABSL4_11460G0001
 1228 Glutamate synthase (ferredoxin)
 0.01102
 0.0703
 0.06278
 0.0399
 UBAL3_95680085
 83